REMARKS

Claims 12, 14-20 and 31-34 are amended. Claim 35 is added. Claims 22-30 have been withdrawn from consideration by the Examiner. Claims 12-14, 16-21 and 31-35 are active and under consideration.

At the outset, Applicants wish to thank Examiner Marvich for the helpful and courteous discussion conducted with their U.S. representative, on March 17, 2009. The supporting remarks for patentability are consistent with the remarks made during the discussion with the Examiner.

Claims 12-15, 19-21 and 31-34 stand rejected under 35 USC 102(b) as being anticipated by _Poquet et al_, J. Bacteriology, 1998, Vol. 180, pages 1904-1912.

However, this reference fails to disclose or suggest the claimed invention.

Notably, _Poquet et al_ (J. Bacteriology, 1998, Vol. 180: 1904-1912) disclose a plasmid pFUN comprising sequence accession number GenBank U95834 which contains the sequence named nlp3 (see attached copy of NCBI description of GenBank U95834). The sequence accession number U95834 consists of:

i) p_{Zn} promoter;

ii)   a sequence encoding ZitR; and

iii)   part of sequence coding for ZitS.

This sequence has been cloned in the polylinker of pFUN as to obtain expression of a fusion peptide n1p3/ΔNuc. Therefore, _Poquet et al_ disclose a plasmid containing the p_{Zn} promoter (promoter sequence corresponding to SEQ ID NO: 1 of claimed expression cassette), a sequence encoding ZitR, the N-terminal part of ZitS fused with the sequence coding for ΔNuc, followed by the downstream restriction sites of the polylinker.

Amended claims 12 and 15 clearly relate to an expression cassette which does not contain

a sequence encoding any part of L. lactis **ZitS**. Consequently, the amended claims are clearly not anticipated by *Poquet et al.*

It is also clear that *Poquet et al* would have failed to have rendered the claimed invention obvious at the time it was made. *Poquet et al* identified among others a sequence (U95834 GenBank sequence) which contains n1p3 coding sequence. *Poquet et al* are only interested in exported peptide n1p3, and are totally silent about a possible function of the other nucleotide sequences contained in U95834 GenBank sequence. Nothing in the disclosure of *Poquet et al* or in accession number U95834 report would have suggested to the artisan that any other sequences contained in U95834 sequence could have a regulating function or code for a protein. See the attached NCBI description of GenBank U95834.

Therefore the person skilled in the art would not have been motivated to isolate specifically the nucleotide sequence corresponding to p_{Zn} promoter and sequence encoding ZitR from sequence GenBank accession number U95834 in order to engineer an expression cassette which has the characteristic to regulate expression of a gene according to the concentration of zinc in the culture medium.

Further, *Poquet et al* would not have enabled one skilled in the art to do so in any event.

Hence, this ground of rejection is unsustainable and should be withdrawn.

Claims 12-21 and 31-34 stand rejected under 35 USC 112, first paragraph, as the present specification ostensibly does not provide enablement for any embodiment of expression cassettes other than that containing SEQ ID NO: 1 operably linked to nucleotides 357-794 of SEQ ID NO: 2 further operably linked to a restriction site.

However, it is believed that the present claims are fully enabled by the present specification for the following reasons. The comments set forth below refer to Annex 1 and Annex 2, copies of

which are attached to this response.

First, the definition "at least 80% identity with the *Lactococcus lactis* ZitR protein GENBANK AAK06214" does not encompass a broad variety of proteins.

Second, Annex 1 shows the results of a BLAST search performed against the nr database which includes all the known protein sequences of all living organisms. Among these sequences, the only ones which share at least 80% identity with ZitR of L. *lactis* subsp. Lactis Il1403 (GenBank AAK06214) are ZitR proteins, namely the ZitR protein of L. *lactis* subsp. *cremoris* MG1363 (88% identity) and the ZitR protein of L. *lactis* subsp. *cremoris* SK11 (89% identity). As a matter of fact there is no protein having at least 80% identity with GenBank AAK06214 which is not a ZitR protein. The next proteins which have the higher homology with ZitR are Streptococcus proteins which have at most 54% identity with GenBank AAK06214. Therefore, it is very unlikely that one can isolate a protein having 80% identity or more with GenBank AAK06214 which is not a ZitR protein.

Annex 2 shows the results of a BLAST search performed against the whole genome sequences of L. *lactis* subsp. Lactis Il1403, L. *lactis* subsp. *cremoris* MG1363 and L. *lactis* subsp. *cremoris* SK11. There is no lactococcal protein, other than the ZitR proteins, having more than 38% identity with GenBank AAK06214.

Therefore using a probe derived from the sequence encoding GenBank AAK06214, or from nucleotides 357 to 794 of SEQ ID NO:9 of the instant application for screening a lactococcal DNA library, one of skill in the art would be able to easily discriminate a sequence encoding a ZitR protein from other lactococcal sequences.

11

Moreover, only the whole genome sequence of L. *lactis* subsp. Lactis Il1403 (which was published in 2001) was available before the invention was made. The genome sequences of *Lactococcus lactis* subsp. *cremoris* SK11 and *Lactococcus lactis* subsp. *cremoris* MG1363 were only available in GenBank in 2006 and 2007 respectively. It is pointed out, however, that besides indicating GenBank AAK06214 as the reference sequence for a ZitR protein, the present application discloses another sequence encoding a ZitR protein, namely nucleotides 357 to 794 of SEQ ID NO:9, which encodes the ZitR protein of *lactis* subsp. *cremoris* MG1363.

Actually, the knowledge of the lactococcal genome sequences is not necessary to practice the claimed invention. As indicated above, one of ordinary skill in the art could have easily obtained polynucleotides encoding lactococcal ZitR proteins by screening a DNA library of a *Lactococcus* with a probe derived from the sequence encoding GenBank AAK06214, or from nucleotides 357 to 794 of SEQ ID NO:9.

BLAST results are provided herewith solely to evidence that the lactococcal genome does not contain any protein having more than 80% identity with GenBank AAK06214 which is not a ZitR protein.

Second, the two BLAST searches and results thereof noted above indicate that the present specification does in fact satisfy both the statutory enablement requirement under 35 USC 112, first paragraph, and the case law tests therefor cited by the Examiner.

Specifically, under the case law tests for enablement articulated in In re Wright and In re Fisher, cited by the Examiner, it is clear that since nucleotide sequences having more than 80% identity with GENBANK AAK06214 could easily be obtained by routine screening with a probe (as described above), undue experimentation would not be required.

Claims 12-16, 18-20 and 31-34 are objected to.

However, in view of the above claim amendments, this ground of rejection is deemed moot.
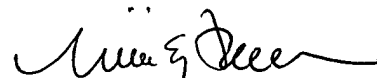
The specification stands objected to.

However, attached to this response is a Substitute Specification which meets the requirements of 37 CFR 1.77(b).

CONCLUSION

Accordingly, in view of all of the above, it is believed that this application is now in condition for allowance. Early notice to this effect is earnestly solicited.

Applicant hereby petitions for the Commissioner to charge any additional fees or any underpayment of fees which may be required to maintain the pendency of this case or credit any overpayment to Deposit Account No. 14-0112.

Respectfully submitted,
THE NATH LAW GROUP

William E. Beaumont
Registration No. 30,996
Customer No. 20529

Date: April 7, 2009
THE NATH LAW GROUP
112 S. West Street
Alexandria, Virginia 22314
Tel: (703) 548-6284
Fax: (703) 683-8396
WEB/get

Search Nucleotide   for   Go   Clear

Limits   Preview/Index   History   Clipboard   Details

Format: **GenBank** FASTA Graphics More Formats▼   Download▼   Save▼   Links▼

GenBank: U95834.1

Lactococcus lactis putative lipoprotein Nlp3 precursor, gene, partial cds

Features Sequence

```
LOCUS       LLU95834               945 bp    DNA
linear   BCT 24-APR-1998
DEFINITION  Lactococcus lactis putative lipoprotein Nlp3
precursor, gene,
            partial cds.
ACCESSION   U95834
VERSION     U95834.1  GI:3043865
KEYWORDS    .
SOURCE      Lactococcus lactis subsp. cremoris MG1363
  ORGANISM  Lactococcus lactis subsp. cremoris MG1363
            Bacteria; Firmicutes; Lactobacillales;
Streptococcaceae;
            Lactococcus.
REFERENCE   1  (bases 1 to 945)
  AUTHORS   Poquet,I., Ehrlich,S.D. and Gruss,A.
  TITLE     An export-specific reporter designed for gram-
positive bacteria:
            application to Lactococcus lactis
  JOURNAL   J. Bacteriol. 180 (7), 1904-1912 (1998)
   PUBMED   9537391
REFERENCE   2  (bases 1 to 945)
  AUTHORS   Poquet,I. and Gruss,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAR-1997) Laboratoire de Genetique
Appliquee-URLGA,
            Institut National de la Recherche Agronomique,
CRJ, Jouy en Josas
            78352, France
FEATURES             Location/Qualifiers
     source          1..945
                     /organism="Lactococcus lactis subsp.
cremoris MG1363"
                     /mol_type="genomic DNA"
                     /strain="MG1363"
                     /db_xref="taxon:416870"
     CDS             complement(<1..330)
                     /note="identified as a fusion to a
signal peptide-less
                     form of the staphylococcal nuclease
reporter which
                     displays nuclease activity; similar to
S. pneumoniae
                     adhesion protein, Swiss-Prot Accession
Number P42363"
```

Change Region Shown

Customize View

Pick Primers
Design and test primers for this
sequence using Primer-BLAST.

**All links from this
record**

Full text in PMC
Protein
PubMed
Taxonomy
Related Sequences

```
                    /codon_start=1
                    /transl_table=11
                    /product="putative lipoprotein Nlp3
precursor"
                    /protein_id="AAC14602.1"
                    /db_xref="GI:3043866"
                    /translation="MKKILMLFAIPAVLLLAGCQKTADKP
EVVTTFEPMYEFTKAIVG

DKVKIENIVPANQEVHEFEPSAKQVATMTNAQAIIYNSDDLEKWALKVNNKGVKIEAS
                    KDVNKIKG"
     sig_peptide        complement(277..330)
                    /note="encodes lipoprotein-type signal
peptide"
     mat_peptide        complement(<1..276)
                    /product="putative lipoprotein Nlp3"
ORIGIN
        1 tcctttaatt ttattgacat ctttgcttgc ttctattttg
actcctttat tattcacttt
       61 cagagcccat ttttcaaggt catcagaatt ataaataata
gcttgagcat ttgtcattgt
      121 tgcaacttgc ttggcactcg gttcaaattc gtgaacttct
tgattcgccg gaacaatatt
      181 ttcaatttta accttatctc caacaatcgc tttcgtaaat
tcatacatcg gctcaaaagt
      241 tgtcacaact tctggtttgt ctgctgtttt ttgacaacca
gcaagaagta aaactgccgg
      301 aatagcaaat aacatcaata ttttcttcat cgaaactcct
ccgtaagtac tgataagaat
      361 tgacttatca ctttttgttc ttcgtcagta aatttgtctc
ctaattcttg gtaggtactt
      421 agagttttct catgatgagc agcatgttct ttagcaactg
gaattgcttt ttctgtcagg
      481 ctccaaagga ctacgcgttc gtcatttgtt gcccgacttg
atttaatcag ttcttgctct
      541 tgtaattttt tgagagcttt agttaccgct gctggcgaaa
tcttgagttg ctcggcaatt
      601 ctcgcgtttg tcgaaacctc tgcagctaga atcattaaga
tatgttcttg cgtgcttgtt
      661 agcttaacat tactttngca ttcgccgagt aatatttcat
gcttgttttn tgcaaactgc
      721 ataattgccc caagaaactg gtcgatttga tttgctaaan
tcatagtatt ttgtcctcca
      781 taattagttt actggttaat tatatagcaa agtaaaaata
atgtcaacca gttaacatta
      841 tttttactt ttttatttga aaaatccttc catccttaag
ccgaacatca aaacaataag
      901 ttttattact aacagtttga ccaccgctag ttgaaccagc tgaca
//
```

BLAST Basic Local Alignment Search Tool

•

Edit and Resubmit Save Search Strategies Formatting options Download

gb|AAK06214| (145 letters)

Results for: gb|AAK06214.1 zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis Il1403](145aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
 gi|12725171|gb|AAK06214.1|AE006439_11
Description
 zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Molecule type
 amino acid
Query Length
 145

Database Name
 nr
Description
 All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program
 BLASTP 2.2.19+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Reference - compositional score matrix adjustment
Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.
Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Mar 2, 2009 5:57 PM
Number of letters	2,739,991,458
Number of sequences	7,946,514
Entrez query	none

Karlin-Altschul statistics

| Params	Ungapped	Gapped
Lambda	0.310848	0.267
K	0.124161	0.041
H	0.32399	0.14

Results Statistics

Length adjustment   109
Effective length of query   36
Effective length of database 1873821432
Effective search space   67457571552
Effective search space used 67457571552

Graphic Summary
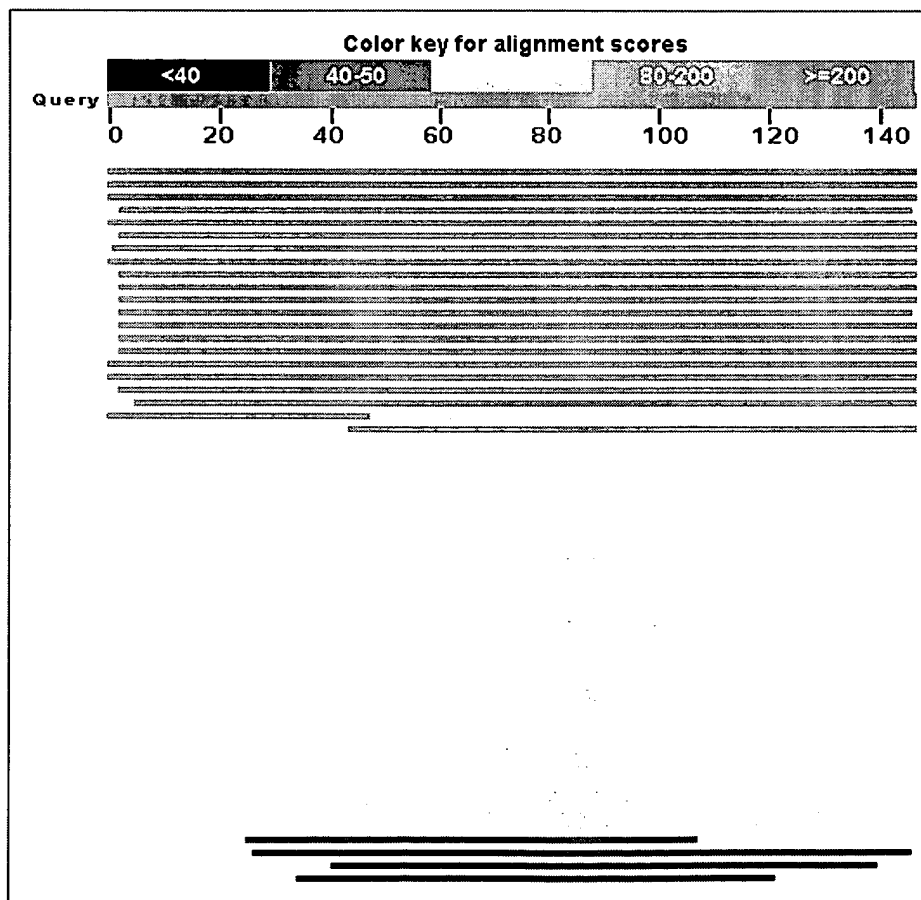Show Conserved Domains
Putative conserved domains have been detected, click on the image below for detailed results.
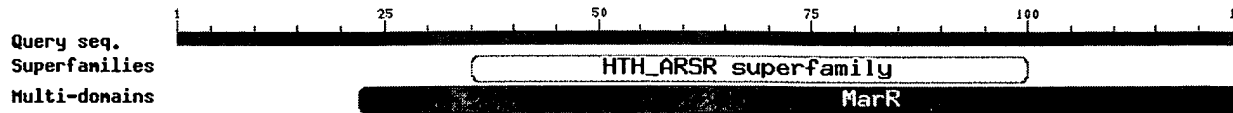
Distribution of 100 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Descriptions

Sequences producing significant alignments:	Score (Bits)	E Value	
ref|NP_268273.1| zinc transport transcription regulator [Lact...	291	1e-77	G
ref|YP_811979.1| transcriptional regulator [Lactococcus lacti...	268	1e-70	G
ref|YP_001033643.1| transcriptional regulator of the zit oper...	267	2e-70	G
ref|YP_001034147.1| multiple antibiotic resistance operon tra...	154	2e-36	G
ref|NP_722293.1| putative transcriptional regulator [Streptoc...	145	1e-33	G
ref|YP_002122498.1| transcriptional repressor AdcR for Zn(2+)...	143	3e-33	G
ref|NP_606407.1| putative repressor protein [Streptococcus py...	141	1e-32	G
ref|ZP_02920004.1| hypothetical protein STRINF_00865 [Strepto...	141	2e-32	
ref|NP_268489.1| putative repressor protein [Streptococcus py...	141	2e-32	G
ref|YP_002561480.1| MarR-family regulatory protein [Streptoco...	138	1e-31	G
ref|NP_687190.1| adc operon repressor AdcR [Streptococcus aga...	136	5e-31	G
ref|YP_001451205.1| repressor protein adcR [Streptococcus gor...	133	4e-30	G
ref|ZP_01817760.1| adc operon repressor AdcR [Streptococcus p...	132	6e-30	
ref|NP_359565.1| adc operon repressor AdcR [Streptococcus pne...	131	2e-29	G
ref|NP_346556.1| adc operon repressor AdcR [Streptococcus pne...	130	2e-29	G
ref|YP_138725.1| zinc transport transcriptional repressor [St...	129	5e-29	G
ref|YP_819746.1| zinc transport transcriptional repressor [St...	128	1e-28	G
ref|YP_001197479.1| transcriptional regulator [Streptococcus ...	116	7e-25	G
ref|ZP_03625066.1| transcriptional regulator, MarR family [St...	110	4e-23	
emb|CAA75313.1| hypothetical protein [Lactococcus lactis subs...	92.4	1e-17	
ref|ZP_00365496.1| COG1846: Transcriptional regulators [Strep...	90.9	3e-17	
ref|YP_001485459.1| MarR family transcriptional regulator [Ba...	67.0	5e-10	G
ref|YP_001199672.1| transcriptional regulator [Streptococcus ...	63.2	6e-09	G
ref|YP_187316.1| MarR family transcriptional regulator [Staph...	63.2	7e-09	G
ref|YP_001777305.1| transcriptional repressor for Zn(2+)-resp...	62.8	8e-09	G
ref|YP_501777.1| hypothetical protein SAOUHSC_02819 [Staphylo...	62.8	8e-09	G
ref|ZP_05563431.1| MarR family transcriptional regulator [Sta...	61.2	3e-08	
ref|YP_174450.1| MarR family transcriptional regulator [Bacil...	60.5	4e-08	G
ref|ZP_080661.1| transcriptional regulator YvnA [Bacillus lic...	59.3	1e-07	G
ref|YP_234603.1| hypothetical protein pSHaeC05 [Staphylococcu...	59.3	1e-07	G
ref|YP_093087.1| YvnA [Bacillus licheniformis ATCC 14580] >gb...	59.3	1e-07	G
ref|ZP_00738634.1| Transcriptional regulator, MarR family [Ba...	55.8	9e-07	
ref|ZP_02613091.1| transcriptional regulator, MarR family [Cl...	54.3	3e-06	
ref|YP_001253547.1| MarR family transcriptional regulator [Cl...	54.3	3e-06	G
ref|YP_001786643.1| MarR family transcriptional regulator [Cl...	54.3	3e-06	G
ref|YP_001053131.1| MarR family transcriptional regulator [La...	53.9	4e-06	G
ref|ZP_02617530.1| transcriptional regulator, MarR family [Cl...	53.9	4e-06	
ref|YP_861960.1| MarR family transcriptional regulator [Grame...	53.9	4e-06	G
ref|NP_391388.1| hypothetical protein BSU35080 [Bacillus subt...	53.5	5e-06	G
ref|ZP_02994615.1| hypothetical protein CLOSPO_01734 [Clostri...	53.5	6e-06	
ref|ZP_01994138.1| hypothetical protein DORLON_00120 [Dorea l...	53.1	6e-06	
ref|ZP_03294054.1| hypothetical protein CLOHIR_02015 [Clostri...	53.1	7e-06	
ref|ZP_02111336.1| hypothetical protein CLOBAR_00939 [Clostri...	52.4	1e-05	
ref|YP_001390364.1| MarR family transcriptional regulator [Cl...	52.4	1e-05	G
ref|YP_001786407.1| MarR family transcriptional regulator [Cl...	51.6	2e-05	G
ref|YP_508775.1| transcriptional regulator [Lactococcus lacti...	51.2	2e-05	G
ref|YP_001689248.1| MarR family transcriptional regulator [Ly...	51.2	3e-05	G
ref|NP_266864.1| transcription regulator [Lactococcus lactis ...	51.2	3e-05	G
ref|ZP_01723095.1| transcriptional regulator, MarR family pro...	50.4	4e-05	
ref|YP_808147.1| transcriptional regulator [Lactococcus lacti...	50.4	5e-05	G
ref|NP_786298.1| transcription regulator [Lactobacillus plant...	50.1	6e-05	G
ref|YP_757477.1| MarR family transcriptional regulator [Maric...	50.1	6e-05	G
ref|NP_391385.1| hypothetical protein BSU35050 [Bacillus subt...	50.1	6e-05	G
ref|NP_111681.1| transcription regulator (SlyA-related) [Ther...	49.7	7e-05	G
ref|NP_419215.1| MarR family transcriptional regulator [Caulo...	49.3	9e-05	G
ref|YP_001031460.1| MarR family transcriptional regulator [La...	49.3	1e-04	G
ref|NP_603576.1| MarR family transcriptional regulator [Fusob...	48.9	1e-04	G
ref|YP_136915.1| MarR family transcriptional regulator [Strep...	48.9	1e-04	G
ref|YP_001165566.1| possible MarR family transcriptional regu...	48.9	1e-04	G
ref|ZP_00144611.1| Transcriptional regulator, MarR family [Fu...	48.9	1e-04	

ref|YP_819912.1|	MarR family transcriptional regulator [Strep...	48.9	1e-04 G
ref|YP_079349.1|	transcriptional regulator YvmB [Bacillus lic...	48.5	2e-04 G
ref|ZP_01219553.1|	putative transcriptional regulator, MarR f...	45.1	2e-04
ref|YP_091766.1|	YvmB [Bacillus licheniformis ATCC 14580] >gb...	48.1	2e-04 G
ref|YP_129221.1|	MarR family transcriptional regulator [Photo...	45.1	2e-04 G
ref|ZP_00990845.1|	hypothetical transcriptional regulator, Ma...	48.1	2e-04
ref|YP_001219891.1|	MarR family transcriptional regulator [Al...	47.8	3e-04 G
ref|YP_001636202.1|	MarR family transcriptional regulator [Le...	47.8	3e-04 G
ref|YP_106511.1|	putative transcriptional regulatory protein ...	47.4	4e-04 G
ref|YP_001961550.1|	Transcriptional regulator, marR family [L...	47.4	4e-04 G
ref|YP_001510724.1|	MarR family transcriptional regulator [Cl...	47.4	4e-04 G
ref|ZP_01065868.1|	hypothetical transcriptional regulator, Ma...	47.0	5e-04
ref|YP_140799.1|	MarR family transcriptional regulator [Strep...	47.0	5e-04 G
ref|YP_143999.1|	MarR family transcriptional regulator [Therm...	46.6	6e-04 G
ref|YP_293371.1|	regulatory protein, MarR [Ralstonia eutropha...	46.6	7e-04 G
ref|YP_001307422.1|	MarR family transcriptional regulator [Cl...	46.6	7e-04 G
ref|ZP_02950515.1|	transcriptional regulator, MarR family [Cl...	46.2	8e-04
ref|NP_266269.1|	transcription regulator [Lactococcus lactis ...	46.2	0.001 G
ref|YP_002252539.1|	transcriptional regulator, MarR family [D...	46.2	0.001 G
ref|ZP_01654255.1|	probable marR-family transcription regulat...	46.2	0.001
ref|YP_773250.1|	MarR family transcriptional regulator [Burkh...	45.8	0.001 G
ref|ZP_01131766.1|	transcriptional regulator, MarR family pro...	45.8	0.001
ref|ZP_00238819.1|	transcriptional regulator, MarR family [Ba...	45.8	0.001
ref|YP_002467440.1|	transcriptional regulator, MarR family [C...	45.8	0.001 G
ref|ZP_03547491.1|	hypothetical protein BLAHAN_01259 [Blautia...	45.4	0.001
ref|ZP_02891041.1|	transcriptional regulator, MarR family [Bu...	45.4	0.001
ref|YP_001808132.1|	MarR family transcriptional regulator [Bu...	45.4	0.001 G
ref|ZP_02906301.1|	transcriptional regulator, MarR family [Bu...	45.4	0.001
ref|ZP_02361996.1|	transcriptional regulator, MarR family pro...	45.4	0.001
ref|NP_977055.1|	MarR family transcriptional regulator [Bacil...	45.4	0.002 G
ref|NP_782475.1|	MarR family transcriptional regulator [Clost...	45.4	0.002 G
ref|ZP_03570809.1|	transcriptional regulator, MarR family [Bu...	45.1	0.002
ref|YP_001119315.1|	MarR family transcriptional regulator [Bu...	45.1	0.002 G
ref|YP_002418276.1|	Histone acetyltransferase HPA2 and relate...	45.1	0.002 G
ref|ZP_02355848.1|	transcriptional regulator, MarR family pro...	45.1	0.002
ref|YP_443075.1|	MarR family transcriptional regulator [Burkh...	44.7	0.002 G
ref|ZP_02633996.1|	transcriptional regulator, MarR family [Cl...	44.7	0.002
ref|YP_001374721.1|	MarR family transcriptional regulator [Ba...	44.7	0.002 G
ref|YP_819461.1|	transcriptional regulator [Leuconostoc mesen...	44.7	0.002 G
ref|ZP_02027443.1|	hypothetical protein EUBVEN_02713 [Eubacte...	44.7	0.003

Alignments **Select All** Get selected sequences Distance tree of results

>**ref|NP_268273.1|** G zinc transport transcription regulator [Lactococcus lactis subsp. lactis Il1403]
 gb|AAK06214.1|AE006439_11 G zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Length=145

 GENE ID: 1115793 zitR | zinc transport transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 291 bits (744), Expect = 1e-77, Method: Compositional matrix adjust.
 Identities = 145/145 (100%), Positives = 145/145 (100%), Gaps = 0/145 (0%)

Query 1   MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
            MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL
Sbjct 1   MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60

Query 61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120
            KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE
Sbjct 61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120

Query 121 LGNKFTDEEQEVISKFLSALTEEFQ 145
            LGNKFTDEEQEVISKFLSALTEEFQ
Sbjct 121 LGNKFTDEEQEVISKFLSALTEEFQ 145

>**ref|YP_811979.1|** G transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 gb|ABJ73866.1| G Transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=145

GENE ID: 4433026 LACR_2420 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 268 bits (685), Expect = 1e-70, Method: Compositional matrix adjust.
 Identities = 130/145 (89%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA ++STNA+IAE+L
Sbjct  1    MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILAAEVSTNARIAEQL  60

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
            KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHA HHEKTLSTYQE
Sbjct  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHAAHHEKTLSTYQE  120

Query  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
            LG+KFTDEEQ+VIS+FLS LTEEF+
Sbjct  121  LGDKFTDEEQKVISQFLSVLTEEFR  145
```

>ref|YP_001033643.1| 🇬 transcriptional regulator of the zit operon [Lactococcus lactis
subsp. cremoris MG1363]
 emb|CAL98965.1| 🇬 transcriptional regulator of the zit operon [Lactococcus lactis
subsp. cremoris MG1363]
Length=145

GENE ID: 4799067 zitR | transcriptional regulator of the zit operon
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 267 bits (682), Expect = 2e-70, Method: Compositional matrix adjust.
 Identities = 129/145 (88%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA ++STNA+IAE+L
Sbjct  1    MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILAAEVSTNARIAEQL  60

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
            KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA+PVAKEHA HHEKTLSTYQE
Sbjct  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAIPVAKEHAAHHEKTLSTYQE  120

Query  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
            LG+KFTDEEQ+VIS+FLS LTEEF+
Sbjct  121  LGDKFTDEEQKVISQFLSVLTEEFR  145
```

>ref|YP_001034147.1| 🇬 multiple antibiotic resistance operon transcriptional repressor
(MarR), putative [Streptococcus sanguinis SK36]
 gb|ABN43597.1| 🇬 Multiple antibiotic resistance operon transcriptional repressor
(MarR), putative [Streptococcus sanguinis SK36]
Length=147

GENE ID: 4806188 adcR | multiple antibiotic resistance operon transcriptional
repressor (MarR), putative [Streptococcus sanguinis SK36]
(10 or fewer PubMed links)

 Score = 154 bits (389), Expect = 2e-36, Method: Compositional matrix adjust.
 Identities = 78/142 (54%), Positives = 102/142 (71%), Gaps = 0/142 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            LA +IDQFL  ++  AEN+HEIL+G C SDV LT+TQEHILMLL+E+  TN+ +A+KL +
Sbjct  4    LAQKIDQFLNEVILKAENQHEILIGSCTSDVPLTNTQEHILMLLSEESLTNSDLAKKLNV  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L QE++++ +   D RV + LTE A P+AKEH HH TL TYQ+L
Sbjct  64   SQAAVTKAVKSLARQEMLQAFKDKRDARVTFYRLTELAQPIAKEHQHHAHTLETYQKLA  123

Query  123  NKFTDEEQEVISKFLSALTEEF  144
            +F+  EQ VI+KFL AL  E
Sbjct  124  EQFSASEQAVIAKFLEALVGEI  145
```

>ref|NP_722293.1| 🇬 putative transcriptional regulator [Streptococcus mutans UA159]
 gb|AAN59599.1|AE015022_6 🇬 putative transcriptional regulator [Streptococcus mutans UA159]
Length=148

GENE ID: 1029245 SMU.1995c | putative transcriptional regulator
[Streptococcus mutans UA159] (10 or fewer PubMed links)

 Score = 145 bits (365), Expect = 1e-33, Method: Compositional matrix adjust.
 Identities = 76/146 (52%), Positives = 105/146 (71%), Gaps = 1/146 (0%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQIS-TNAKIAEK  59
            M+L  QID  + I+  AEN HE+L+G C+SDVKLT+TQEHILMLL+++ S TN+ +A++
Sbjct  1    MTLGQQIDALINQIILKAENHHELLIGSCQSDVKLTNTQEHILMLLSQEKSLTNSDLAKE  60

Query  60   LKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQ  119
            L IS AAVTKA+K L  QE+++  +   D RV + LT+ A PVAKEH HH  TLS Y
Sbjct  61   LNISQAAVTKAVKSLVGQEMLELIKDGTDARVTYFRLTKLAEPVAKEHEHHHVATLSVYD  120

Query  120  ELGNKFTDEEQEVISKFLSALTEEFQ  145
            +  KF+ +E+ VIS+FL+ALT+E +
Sbjct  121  RISQKFSQKEKSVISRFLTALTKELE  146
```

```
>ref|YP_002122498.1| G transcriptional repressor AdcR for Zn(2+)-responsive expression
[Streptococcus equi subsp. zooepidemicus MGCS10565]
  gb|ACG61485.1| G transcriptional repressor AdcR for Zn(2+)-responsive expression
[Streptococcus equi subsp. zooepidemicus MGCS10565]
Length=147

 GENE ID: 6760627 adcR | transcriptional repressor AdcR for Zn(2+)-responsive
expression [Streptococcus equi subsp. zooepidemicus MGCS10565]

  Score = 143 bits (361), Expect = 3e-33, Method: Compositional matrix adjust.
  Identities = 70/143 (48%), Positives = 102/143 (71%), Gaps = 0/143 (0%)

Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            L ++D + I+ AEN+HE+L G C+SDVKLT+TQEHILMLL+++ TN +A++L I
Sbjct  4    LEKKLDNLVNRILLKAENQHELLFGACQSDVKLTNTQEHILMLLSQEKLTNTDLAKRLNI  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L +QE++ ++ T D RV + LT+ A P+AKEH HH+KTL+ Y L
Sbjct  64   SQAAVTKAIKGLIKQEMLAGTKDTVDARVTYFELTDLARPIAKEHTHHHDKTLAVYHRLL  123

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
               F+ EEQ ++ KF++A +EE +
Sbjct  124  AHFSAEEQVIVEKFITAFSEELE  146


>ref|NP_606407.1| G putative repressor protein [Streptococcus pyogenes MGAS8232]
  ref|NP_663873.1| G putative repressor protein [Streptococcus pyogenes MGAS315]
  ref|NP_801332.1| G putative repressor protein [Streptococcus pyogenes SSI-1]
  20 more sequence titles

  ref|YP_059443.1| G MarR family transcriptional regulator [Streptococcus pyogenes
MGAS10394]
  ref|YP_279544.1| G MarR family transcriptional regulator [Streptococcus pyogenes
MGAS6180]
  ref|YP_595809.1| G MarR family transcriptional regulator [Streptococcus pyogenes
MGAS9429]
  ref|YP_597688.1| G MarR family transcriptional regulator [Streptococcus pyogenes
MGAS10270]
  ref|YP_599676.1| G MarR family transcriptional regulator [Streptococcus pyogenes
MGAS2096]
  ref|YP_601578.1| G Transcriptional regulator, MarR family [Streptococcus pyogenes
MGAS10750]
  ref|YP_001127671.1| G MarR family regulatory protein [Streptococcus pyogenes str. Manfredo]
  ref|YP_002285129.1| G Putative repressor protein [Streptococcus pyogenes NZ131]
  sp|Q5XEA3.1|ADCR_STRP6  RecName: Full=Transcriptional repressor adcR
  gb|AAL96906.1| G putative repressor protein [Streptococcus pyogenes MGAS8232]
  gb|AAM78676.1| G putative repressor protein [Streptococcus pyogenes MGAS315]
  dbj|BAC63165.1| G putative repressor protein [Streptococcus pyogenes SSI-1]
  gb|AAT86260.1| G Transcriptional regulator, MarR family [Streptococcus pyogenes
MGAS10394]
  gb|AAX71189.1| G transcriptional regulator, MarR family [Streptococcus pyogenes
MGAS6180]
  gb|ABF31265.1| G transcriptional regulator, MarR family [Streptococcus pyogenes
MGAS9429]
  gb|ABF33144.1| G Transcriptional regulator, MarR family [Streptococcus pyogenes
MGAS10270]
  gb|ABF35132.1| G Transcriptional regulator, MarR family [Streptococcus pyogenes
MGAS2096]
  gb|ABF37034.1| G Transcriptional regulator, MarR family [Streptococcus pyogenes
MGAS10750]
  emb|CAM29417.1| G MarR-family regulatory protein [Streptococcus pyogenes str. Manfredo]
  gb|ACI60434.1| G Putative repressor protein [Streptococcus pyogenes NZ131]
Length=147

 GENE ID: 994164 adcR | putative repressor protein
[Streptococcus pyogenes MGAS8232] (10 or fewer PubMed links)

  Score = 141 bits (356), Expect = 1e-32, Method: Compositional matrix adjust.
  Identities = 69/144 (47%), Positives = 101/144 (70%), Gaps = 0/144 (0%)

Query  2    SLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLK  61
            +L ++D + TI+ AEN+HE+L G C+SDVKLT+TQEHILMLL++Q TN +A+ L
Sbjct  3    TLEKKLDNLVNTILLKAENQHELLFGACQSDVKLTNTQEHILMLLSQQRLTNTDLAKALN  62

Query  62   ISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQEL  121
            IS AAVTKA+K L +Q+++ ++ T D RV + LTE A P+A EH HH++TL+ Y L
Sbjct  63   ISQAAVTKAIKSLVKQDMLAGTKDTVDARVTYFELTELAKPIASEHTHHHDETLNVYNRL  122

Query  122  GNKFTDEEQEVISKFLSALTEEFQ  145
              KF+ +E E++ KF++ EE +
Sbjct  123  LQKFSAKELEIVDKFVTVFAEELE  146


>ref|ZP_02920004.1| hypothetical protein STRINF_00865 [Streptococcus infantarius
```

subsp. infantarius ATCC BAA-102]
 gb|EDT48012.1| hypothetical protein STRINF_00865 [Streptococcus infantarius
subsp. infantarius ATCC BAA-102]
Length=148

```
 Score = 141 bits (355),  Expect = 2e-32, Method: Compositional matrix adjust.
 Identities = 70/145 (48%), Positives = 103/145 (71%), Gaps = 0/145 (0%)

Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            M L  QID + I+  AEN+HE+L G C+S V+LT+TQEHILMLL+++  TN+ +A++L
Sbjct  1    MQLEKQIDCLVNEILLKAENQHELLFGACQSGVELTNTQEHILMLLSQERLTNSALAKRL  60

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
            IS AAVTKA+K L ++ ++   + +D RV  + LTE A PVA EH  HH   TLS Y++
Sbjct  61   NISQAAVTKAIKCLVKEGMLAPVKNKDDARVTYFELTEFAKPVADEHNHHHHATLSVYKK  120

Query  121  LGNKFTDEEQEVISKFLSALTEEFQ  145
            + + F+DEEQ +IS+FL+A ++E +
Sbjct  121  MIDDFSDEEQSIISRFLTAFSDELE  145
```


>ref|NP_268489.1| [G] putative repressor protein [Streptococcus pyogenes M1 GAS]
 ref|YP_281441.1| [G] MarR family transcriptional regulator [Streptococcus pyogenes
MGAS5005]
 gb|AAK33210.1| [G] putative repressor protein [Streptococcus pyogenes M1 GAS]
 gb|AAZ50696.1| [G] transcriptional regulator, MarR family [Streptococcus pyogenes
MGAS5005]
Length=147

 GENE ID: 900432 adcR | putative repressor protein
[Streptococcus pyogenes M1 GAS] (10 or fewer PubMed links)

```
 Score = 141 bits (355),  Expect = 2e-32, Method: Compositional matrix adjust.
 Identities = 69/143 (48%), Positives = 100/143 (69%), Gaps = 0/143 (0%)

Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            L  ++D + TI+  AEN+HE+L G C+SDVKLT+TQEHILMLL++Q  TN +A+ L I
Sbjct  4    LEKKLDNLVNTILLKAENQHELLFGACQSDVKLTNTQEHILMLLSQQRLTNTDLAKALNI  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L +Q+++  ++ T D RV  + LTE A P+A EH  HH++TL+ Y   L
Sbjct  64   SQAAVTKAIKSLVKQDMLAGTKDTVDARVTYFELTELAKPIASEHTHHHDETLNVYNRLL  123

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
            KF+ +E E++ KF++   EE +
Sbjct  124  QKFSAKELEIVDKFVTVFAEELE  146
```


>ref|YP_002561480.1| [G] MarR-family regulatory protein [Streptococcus uberis 0140J]
 emb|CAR40515.1| [G] MarR-family regulatory protein [Streptococcus uberis 0140J]
Length=147

 GENE ID: 7392663 SUB0110 | MarR-family regulatory protein
[Streptococcus uberis 0140J]

```
 Score = 138 bits (348),  Expect = 1e-31, Method: Compositional matrix adjust.
 Identities = 69/143 (48%), Positives = 102/143 (71%), Gaps = 0/143 (0%)

Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            L ++IDQ +  I+  AEN+HE+L G C+S VKLT+TQEHILMLL+++  TN  +A+KL I
Sbjct  4    LESKIDQLVNQILLKAENQHELLFGACQSHVKLTNTQEHILMLLSQEQLTNTDLAKKLNI  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L + E++ + + T D RV  + LT  A P+A+EH  HH++TL+ Y +L
Sbjct  64   SQAAVTKAIKSLMKHEMLSAIKDTVDARVTYFELTPAAKPIAEEHTQHHDETLNVYTKLL  123

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
            + F+ EE+ VI KFL+  ++E +
Sbjct  124  SSFSSEEKAVIDKFLTVFSDELE  146
```


>ref|NP_687190.1| [G] adc operon repressor AdcR [Streptococcus agalactiae 2603V/R]
 ref|NP_734620.1| [G] adc operon repressor AdcR [Streptococcus agalactiae NEM316]
 ref|YP_328885.1| [G] adc operon repressor AdcR [Streptococcus agalactiae A909]
 13 more sequence titles

ref|ZP_00781732.1| repressor protein adcR [Streptococcus agalactiae 18RS21]
 ref|ZP_00784062.1| adc operon repressor AdcR [Streptococcus agalactiae H36B]
 ref|ZP_00786322.1| adc operon repressor AdcR [Streptococcus agalactiae COH1]
 ref|ZP_00787320.1| adc operon repressor AdcR [Streptococcus agalactiae CJB111]
 ref|ZP_00790981.1| adc operon repressor AdcR [Streptococcus agalactiae 515]
 gb|AAM99062.1|AE014198_10 [G] adc operon repressor AdcR [Streptococcus agalactiae 2603V/R]
 emb|CAD45795.1| [G] unknown [Streptococcus agalactiae NEM316]
 gb|ABA46120.1| [G] adc operon repressor AdcR [Streptococcus agalactiae A909]
 gb|EAO61676.1| repressor protein adcR [Streptococcus agalactiae 18RS21]
 gb|EAO70283.1| adc operon repressor AdcR [Streptococcus agalactiae 515]
 gb|EAO73974.1| adc operon repressor AdcR [Streptococcus agalactiae CJB111]
 gb|EAO74935.1| adc operon repressor AdcR [Streptococcus agalactiae COH1]
 gb|EAO77202.1| adc operon repressor AdcR [Streptococcus agalactiae H36B]
Length=147

GENE ID: 1012928 adcR | adc operon repressor AdcR
[Streptococcus agalactiae 2603V/R] (10 or fewer PubMed links)

Score = 136 bits (343), Expect = 5e-31, Method: Compositional matrix adjust.
Identities = 65/143 (45%), Positives = 99/143 (69%), Gaps = 0/143 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            L ++D + I+  AEN+HE+L G C+SDVKLT+TQEHILMLL+++  TN+ +A+KL I
Sbjct  4    LEQKLDHLVSQILLKAENQHELLFGTCQSDVKLTNTQEHILMLLSQEQLTNSDLAKKLNI  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L  Q+++K+++ + D R+ + L+E A P+A EH  HH+ TL  Y  L
Sbjct  64   SQAAVTKAVKSLISQDMLKANKDSKDARITYFELSELAKPIADEHTHHHDNTLGVYGRLV  123

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
            N F+ +E+ V+ +FL   + E +
Sbjct  124  NHFSKDEKVVLERFLDLFSRELE  146
```

>ref|YP_001451205.1| [G] repressor protein adcR [Streptococcus gordonii str. Challis substr. CH1]
 gb|AAO43167.1| putative transcriptional repressor; AdcR [Streptococcus gordonii subsp. challis]
 gb|ABV10972.1| [G] repressor protein adcR [Streptococcus gordonii str. Challis substr. CH1]
Length=147

GENE ID: 5599115 adcR | repressor protein adcR
[Streptococcus gordonii str. Challis substr. CH1] (10 or fewer PubMed links)

Score = 133 bits (335), Expect = 4e-30, Method: Compositional matrix adjust.
Identities = 75/142 (52%), Positives = 101/142 (71%), Gaps = 0/142 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            LA++ID FL  I+  AEN+HEIL+G C S+V LT+TQEHILMLLAE++ TN+ +A+KL +
Sbjct  4    LAHKIDSFLNEIILKAENQHEILVGSCTSNVALTNTQEHILMLLAEEMLTNSDLAKKLNV  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L Q ++++ +   D RV + LTE A P+A EH  HH  TL TYQ L
Sbjct  64   SQAAVTKAVKSLINQGMLETFKDKKDARVTFYRLTELAQPIADEHEHHHAHTLETYQSLL  123

Query  123  NKFTDEEQEVISKFLSALTEEF  144
            ++F+ +EQ+ I KFL AL  E
Sbjct  124  DRFSQDEQQAIEKFLEALVGEI  145
```

>ref|ZP_01817760.1| adc operon repressor AdcR [Streptococcus pneumoniae SP3-BS71]
 ref|YP_002512031.1| [G] MarR-family regulatory protein [Streptococcus pneumoniae ATCC 700669]
 gb|EDK74363.1| adc operon repressor AdcR [Streptococcus pneumoniae SP3-BS71]
 emb|CAR69937.1| [G] MarR-family regulatory protein [Streptococcus pneumoniae ATCC 700669]
Length=146

Score = 132 bits (333), Expect = 6e-30, Method: Compositional matrix adjust.
Identities = 71/143 (49%), Positives = 106/143 (74%), Gaps = 0/143 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
            LA  ID FL  ++  AEN+HEIL+G C S+V LT+TQEHILMLL+E+  TN+++A +L +
Sbjct  4    LAKDIDAFLNEVILQAENQHEILIGHCTSEVALTNTQEHILMLLSEESLTNSELARRLNV  63

Query  63   SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
            S AAVTKA+K L ++ ++++S+ + D RV+ + LT+ A P+A+EH  HHE TL TY+++
Sbjct  64   SQAAVTKAIKSLVKEGMLETSKDSKDARVIFYQLTDLARPIAEEHHHHHEHTLLTYEQVA  123

Query  123  NKFTDEEQEVISKFLSALTEEFQ  145
            +FT  EQ+VI +FL+AL  E +
Sbjct  124  TQFTPNEQKVIQRFLTALVGEIK  146
```

>ref|NP_359569.1| [G] adc operon repressor AdcR [Streptococcus pneumoniae R6]
 ref|ZP_01825537.1| Transcriptional repressor for Zn(2+)-responsive expression [Streptococcus pneumoniae SP11-BS70]
 ref|YP_001836857.1| [G] adc operon repressor AdcR [Streptococcus pneumoniae CGSP14]
 ref|ZP_02964427.1| putative transcriptional repressor [Streptococcus pneumoniae CDC0288-04]
 gb|AAL00780.1| [G] Transcriptional repressor for Zn(2+)-responsive expression [Streptococcus pneumoniae R6]
 gb|EDK63077.1| Transcriptional repressor for Zn(2+)-responsive expression [Streptococcus pneumoniae SP11-BS70]
 gb|ACB91392.1| [G] adc operon repressor AdcR [Streptococcus pneumoniae CGSP14]
 gb|EDT94590.1| putative transcriptional repressor [Streptococcus pneumoniae CDC0288-04]
Length=166

GENE ID: 933868 adcR | adc operon repressor AdcR [Streptococcus pneumoniae R6]
(10 or fewer PubMed links)

Score = 131 bits (329), Expect = 2e-29, Method: Compositional matrix adjust.
Identities = 70/143 (48%), Positives = 106/143 (74%), Gaps = 0/143 (0%)

```
Query  3    LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
```

```
             LA I+ FL  ++  AEN+HEIL+G C S+V LT+TQEHILMLL+E+  TN+++A +L +
Sbjct  24    LAKDINAFLNEVILQAENQHEILIGHCTSEVALTNTQEHILMLLSEESLTNSELARRLNV  83

Query  63    SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
             S AAVTKA+K L ++ ++++S+ + D RV+ + LT+ A P+A+EH  HHE TL TY+++
Sbjct  84    SQAAVTKAIKSLVKEGMLETSKDSKDARVIFYQLTDLARPIAEEHHHHHEHTLLTYEQVA  143

Query  123   NKFTDEEQEVISKFLSALTEEFQ  145
             +FT  EQ+VI +FL+AL  E +
Sbjct  144   TQFTPNEQKVIQRFLTALVGEIK  166
```

>ref|NP_346586.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae TIGR4]

 ref|ZP_01408975.1| **G** hypothetical protein SpneT_02000553 [Streptococcus pneumoniae TIGR4]

 ref|YP_817386.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae D39]
29 more sequence titles

ref|ZP_01820229.1| adc operon repressor AdcR [Streptococcus pneumoniae SP6-BS73]
 ref|ZP_01821749.1| adc operon repressor AdcR [Streptococcus pneumoniae SP9-BS68]
 ref|ZP_01827937.1| adc operon repressor AdcR [Streptococcus pneumoniae SP14-BS69]
 ref|ZP_01830531.1| adc operon repressor AdcR [Streptococcus pneumoniae SP18-BS74]
 ref|ZP_01833186.1| adc operon repressor AdcR [Streptococcus pneumoniae SP19-BS75]
 ref|ZP_01835060.1| adc operon repressor AdcR [Streptococcus pneumoniae SP23-BS72]
 ref|ZP_02708953.1| putative transcriptional repressor [Streptococcus pneumoniae CDC1873-00]
 ref|ZP_02710784.1| putative transcriptional repressor [Streptococcus pneumoniae CDC1087-00]
 ref|ZP_02713441.1| putative transcriptional repressor [Streptococcus pneumoniae SP195]
 ref|ZP_02718213.1| putative transcriptional repressor [Streptococcus pneumoniae CDC3059-06]
 ref|ZP_02721950.1| putative transcriptional repressor [Streptococcus pneumoniae MLV-016]

 ref|YP_001695528.1| **G** putative transcriptional repressor [Streptococcus pneumoniae Hungary19A-6]

 ref|YP_002038763.1| **G** transcriptional regulator, MarR family [Streptococcus pneumoniae G54]
 emb|CAA96184.1| AdcR protein [Streptococcus pneumoniae]

 gb|AAK76226.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae TIGR4]

 gb|ABJ54931.1| **G** adc operon repressor AdcR [Streptococcus pneumoniae D39]
 gb|EDK65765.1| adc operon repressor AdcR [Streptococcus pneumoniae SP14-BS69]
 gb|EDK68416.1| adc operon repressor AdcR [Streptococcus pneumoniae SP18-BS74]
 gb|EDK70926.1| adc operon repressor AdcR [Streptococcus pneumoniae SP19-BS75]
 gb|EDK76701.1| adc operon repressor AdcR [Streptococcus pneumoniae SP6-BS73]
 gb|EDK80035.1| adc operon repressor AdcR [Streptococcus pneumoniae SP9-BS68]
 gb|EDK81745.1| adc operon repressor AdcR [Streptococcus pneumoniae SP23-BS72]

 gb|ACA36761.1| **G** putative transcriptional repressor [Streptococcus pneumoniae Hungary19A-6]
 gb|EDT50754.1| putative transcriptional repressor [Streptococcus pneumoniae CDC1873-00]
 gb|EDT91227.1| putative transcriptional repressor [Streptococcus pneumoniae CDC1087-00]
 gb|EDT92758.1| putative transcriptional repressor [Streptococcus pneumoniae SP195]
 gb|EDT96372.1| putative transcriptional repressor [Streptococcus pneumoniae CDC3059-06]
 gb|EDT98576.1| putative transcriptional repressor [Streptococcus pneumoniae MLV-016]

 gb|ACF56415.1| **G** transcriptional regulator, MarR family [Streptococcus pneumoniae G54]
Length=146

 GENE ID: 931929 SP_2172 | adc operon repressor AdcR
[Streptococcus pneumoniae TIGR4] (10 or fewer PubMed links)

 Score = 130 bits (328), Expect = 2e-29, Method: Compositional matrix adjust.
 Identities = 70/143 (48%), Positives = 106/143 (74%), Gaps = 0/143 (0%)

```
Query  3     LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI  62
             LA I+ FL  ++  AEN+HEIL+G C S+V LT+TQEHILMLL+E+  TN+++A +L +
Sbjct  4     LAKDINAFLNEVILQAENQHEILIGHCTSEVALTNTQEHILMLLSEESLTNSELARRLNV  63

Query  63    SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG  122
             S AAVTKA+K L ++ ++++S+ + D RV+ + LT+ A P+A+EH  HHE TL TY+++
Sbjct  64    SQAAVTKAIKSLVKEGMLETSKDSKDARVIFYQLTDLARPIAEEHHHHHEHTLLTYEQVA  123

Query  123   NKFTDEEQEVISKFLSALTEEFQ  145
             +FT  EQ+VI +FL+AL  E +
Sbjct  124   TQFTPNEQKVIQRFLTALVGEIK  146
```

>ref|YP_138725.1| **G** zinc transport transcriptional repressor [Streptococcus thermophilus LMG 18311]

 ref|YP_140614.1| **G** zinc transport transcriptional repressor [Streptococcus thermophilus CNRZ1066]

 gb|AAV59910.1| **G** zinc transport transcriptional repressor [Streptococcus thermophilus LMG 18311]

 gb|AAV61799.1| **G** zinc transport transcriptional repressor [Streptococcus thermophilus CNRZ1066]

Length=151

GENE ID: 3164452 adcR | zinc transport transcriptional repressor
[Streptococcus thermophilus LMG 18311] (10 or fewer PubMed links)

Score = 129 bits (325), Expect = 5e-29, Method: Compositional matrix adjust.
Identities = 62/145 (42%), Positives = 104/145 (71%), Gaps = 0/145 (0%)

```
Query   1   MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL   60
            + L  Q++Q +  I+   AEN++E+L+G+C S VKLT+TQEHILMLL+E    TN+++A+ L
Sbjct   6   IELEEQVNQLINQILLKAENQYELLIGQCRSKVKLTNTQEHILMLLSEGQKTNSELAKAL   65

Query   61  KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE   120
            +S AAVTKA+K L ++ +++  +  +D RV  + LT++A P+A+EH  HH++TL  Y+
Sbjct   66  NVSQAAVTKAVKTLVKEGMLEGKKDKDDGRVTYFVLTQEAQPIAQEHKEHHQETLGVYRS   125

Query   121 LGNKFTDEEQEVISKFLSALTEEFQ   145
            +  ++F  +E++VI +FL  L E+ +
Sbjct   126 VLDQFDHQERQVIGRFLIKLAEKIE   150
```

>ref|YP_819746.1| [G] zinc transport transcriptional repressor [Streptococcus thermophilus
LMD-9]

gb|ABJ65550.1| [G] transcriptional regulator, MarR family [Streptococcus thermophilus
LMD-9]
Length=147

GENE ID: 4438531 STER_0233 | zinc transport transcriptional repressor
[Streptococcus thermophilus LMD-9] (10 or fewer PubMed links)

Score = 128 bits (322), Expect = 1e-28, Method: Compositional matrix adjust.
Identities = 61/145 (42%), Positives = 104/145 (71%), Gaps = 0/145 (0%)

```
Query   1   MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL   60
            + L  +++Q +  I+   AEN++E+L+G+C S VKLT+TQEHILMLL+E    TN+++A+ L
Sbjct   2   IELEERVNQLINQILLKAENQYELLIGQCRSKVKLTNTQEHILMLLSEGQKTNSELAKAL   61

Query   61  KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE   120
            +S AAVTKA+K L ++ +++  +  +D RV  + LT++A P+A+EH  HH++TL  Y+
Sbjct   62  NVSQAAVTKAVKTLVKEGMLEGKKDKDDGRVTYFVLTQEAQPIAQEHKEHHQETLGVYRS   121

Query   121 LGNKFTDEEQEVISKFLSALTEEFQ   145
            +  ++F  +E++VI +FL  L E+ +
Sbjct   122 VLDQFDHQERQVIGRFLIKLAEKIE   146
```

>ref|YP_001197479.1| [G] transcriptional regulator [Streptococcus suis 05ZYH33]

gb|ABP89079.1| [G] Transcriptional regulator [Streptococcus suis 05ZYH33]
Length=149

GENE ID: 5099418 SSU05_0109 | transcriptional regulator
[Streptococcus suis 05ZYH33] (10 or fewer PubMed links)

Score = 116 bits (290), Expect = 7e-25, Method: Compositional matrix adjust.
Identities = 70/143 (48%), Positives = 100/143 (69%), Gaps = 0/143 (0%)

```
Query   3   LANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKI   62
            +A +I+++L  I+   +EN+ EIL+G C+S VKLT+TQEHILML+ +    TN +IA+++ +
Sbjct   6   IALEIEKYLHEIVLSSENQLEILVGSCQSTVKLTNTQEHILMLIEKAAYTNTEIAKELNV   65

Query   63  SPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELG   122
            S AA+TKA K L  Q L+ + R   D R+V +SLTE A P+A EHA HH  TL  Y+EL
Sbjct   66  SQAAITKATKSLVAQGLLVAVRDDKDARIVRFSLTEAAKPIAAEHAHHHAHTLEAYEELL   125

Query   123 NKFTDEEQEVISKFLSALTEEFQ   145
            ++ EEQE I++FLS L E+ +
Sbjct   126 ENYSLEEQESIARFLSELVEKIR   148
```

>ref|ZP_03625066.1| transcriptional regulator, MarR family [Streptococcus suis 89/1591]
gb|EEF64628.1| transcriptional regulator, MarR family [Streptococcus suis 89/1591]
Length=149

Score = 110 bits (275), Expect = 4e-23, Method: Compositional matrix adjust.
Identities = 69/140 (49%), Positives = 98/140 (70%), Gaps = 0/140 (0%)

```
Query   6   QIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPA   65
            +I+++L  I+   +EN+ EIL+G C+S VKLT+TQEHILML+ +    TN +IA++L +
Sbjct   9   EIEKYLHEIVLSSENQLEILVGSCQSTVKLTNTQEHILMLIEKAAYTNTEIAKELNVSQA   68

Query   66  AVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKF   125
            A+TKA K L  Q L+ + R   D R+V +SLTE A P+A EHA HH  TL  Y+EL    +
Sbjct   69  AITKATKSLVAQGLLVAVRDDKDARIVRFSLTEAAKPIATEHAHHHAHTLEAYEELLEHY   128

Query   126 TDEEQEVISKFLSALTEEFQ   145
            + EEQE I++FLS L E+ +
Sbjct   129 SLEEQESIARFLSELVEKIR   148
```

>emb|CAA75313.1| hypothetical protein [Lactococcus lactis subsp. cremoris]
Length=48

Score = 92.4 bits (228), Expect = 1e-17, Method: Compositional matrix adjust.
Identities = 43/47 (91%), Positives = 46/47 (97%), Gaps = 0/47 (0%)

```
Query   1   MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLA   47
            MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA
Sbjct   1   MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILA   47
```

>ref|ZP_00365496.1| COG1846: Transcriptional regulators [Streptococcus pyogenes M49
591]
Length=103

```
 Score = 90.9 bits (224),  Expect = 3e-17, Method: Compositional matrix adjust.
 Identities = 45/102 (44%), Positives = 68/102 (66%), Gaps = 0/102 (0%)

Query   44   MLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPV   103
             MLL++Q  TN  +A+ L IS AAVTKA+K L +Q+++  ++ T D RV  + LTE A P+
Sbjct   1    MLLSQQRLTNTDLAKALNISQAAVTKAIKSLVKQDMLAGTKDTVDARVTYFELTELAKPI   60

Query   104  AKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ   145
             A EH  HH++TL+ Y  L  KF+ +E E++ KF++    EE +
Sbjct   61   ASEHTHHHDETLNVYNRLLQKFSAKELEIVDKFVTVFAEELE   102
```

>ref|YP_001485459.1| ⬛ MarR family transcriptional regulator [Bacillus pumilus SAFR-032]
  ref|ZP_03056081.1| YvnA [Bacillus pumilus ATCC 7061]
  gb|ABV60899.1| ⬛ possible MarR family transcriptional regulator [Bacillus pumilus
SAFR-032]
  gb|EDW20313.1| YvnA [Bacillus pumilus ATCC 7061]
Length=152

 GENE ID: 5619427 BPUM_0200 | MarR family transcriptional regulator
[Bacillus pumilus SAFR-032] (10 or fewer PubMed links)

```
 Score = 67.0 bits (162),  Expect = 5e-10, Method: Compositional matrix adjust.
 Identities = 40/111 (36%), Positives = 66/111 (59%), Gaps = 2/111 (1%)

Query   36   TSTQEHILMLLAEQI--STNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL   93
             T TQ HIL ++        S N  ++++LK+S  A+TKA+KKL ++ ++       D++ V
Sbjct   42   TLTQLHILSMIQANPNESNNTFLSQQLKLSKPAITKAVKKLIDKGMVDYCHRQGDKKSVY   101

Query   94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF   144
             +SLTEK   +A H  HEK +++Y E   +F  ++ +VI +FL A   E+
Sbjct   102  YSLTEKGTQLAALHDELHEKAVASYLEFLQQFHEDELQVIERFLKAWKEKI   152
```

>ref|YP_001199672.1| ⬛ transcriptional regulator [Streptococcus suis 98HAH33]
  gb|ABP91272.1| ⬛ Transcriptional regulator [Streptococcus suis 98HAH33]
Length=87

 GENE ID: 5101832 SSU98_0112 | transcriptional regulator
[Streptococcus suis 98HAH33] (10 or fewer PubMed links)

```
 Score = 63.2 bits (152),  Expect = 6e-09, Method: Compositional matrix adjust.
 Identities = 41/86 (47%), Positives = 56/86 (65%), Gaps = 0/86 (0%)

Query   60   LKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQ   119
             + +S AA+TKA K L  Q L+ + R    D R+V +SLTE A P+A EHA HH   TL  Y+
Sbjct   1    MNVSQAAITKATKSLVAQGLLVAVRDDKDARIVRFSLTEAAKPIAAEHAHHHAHTLEAYE   60

Query   120  ELGNKFTDEEQEVISKFLSALTEEFQ   145
             EL    ++ EEQE I++FLS L E+ +
Sbjct   61   ELLENYSLEEQESIARFLSELVEKIR   86
```

>ref|YP_187318.1| ⬛ MarR family transcriptional regulator [Staphylococcus aureus
subsp. aureus COL]
  ref|YP_495086.1| ⬛ MarR family transcriptional regulator [Staphylococcus aureus
subsp. aureus USA300]
  ref|YP_001576367.1| ⬛ MarR family transcriptional regulator [Staphylococcus aureus
subsp. aureus USA300_TCH1516]
  ref|ZP_02761767.1| ⬛ MarR family transcriptional regulator [Staphylococcus aureus
subsp. aureus USA300_TCH1516]
  gb|AAW37302.1| ⬛ transcriptional regulator, MarR family [Staphylococcus aureus
subsp. aureus COL]
  gb|ABD21126.1| ⬛ transcriptional regulator, MarR family [Staphylococcus aureus
subsp. aureus USA300_FPR3757]
  gb|ABX30488.1| ⬛ MarR family transcriptional regulator [Staphylococcus aureus
subsp. aureus USA300_TCH1516]
Length=154

 GENE ID: 3238188 SACOL2524 | MarR family transcriptional regulator
[Staphylococcus aureus subsp. aureus COL] (10 or fewer PubMed links)

```
 Score = 63.2 bits (152),  Expect = 7e-09, Method: Compositional matrix adjust.
 Identities = 40/112 (35%), Positives = 66/112 (58%), Gaps = 1/112 (0%)

Query   35   LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL   93
             L+ TQ HI+ L+      N K  ++E L +S  A+TK++KKL  +  L  S    N++R V
Sbjct   36   LSLTQFHIIELIDNNDKVNNKFLSEMLNVSKPAITKSIKKLLAKDLVVESHNEFNKREVN   95

Query   94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ   145
             +SLT+K   ++  H  HEK++ Y+E+   F D+E  VI +FL+    EE +
Sbjct   96   YSLTQKGKKLSYIHDELHEKSVKKYEEVLKVFDDDEMAVIIEFLNRSIEELK   147
```

>ref|YP_001727325.1| transcriptional repressor for Zn(2+)-responsive expression [Leuconostoc citreum KM20]

  gb|ACA81881.1| Transcriptional repressor for Zn(2+)-responsive expression [Leuconostoc citreum KM20]
Length=146

  GENE ID: 6063203 adcR | transcriptional repressor for Zn(2+)-responsive expression [Leuconostoc citreum KM20] (10 or fewer PubMed links)

  Score = 62.8 bits (151), Expect = 8e-09, Method: Compositional matrix adjust.
  Identities = 41/138 (29%), Positives = 72/138 (52%), Gaps = 2/138 (1%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL  60
            MS ++ I Q L T +Q      E + + + K+ +TQ H+LMLL Q +TN+ +AE +
Sbjct  1    MSQSDHIIQELNTFVQTYAASSEFI--QTTAAQKINATQAHLLMLLKTQHATNSSLAESM  58

Query  61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE  120
            ++  A+TKA+K L   + +++ ND+R V + L+ + + +A +H   H
Sbjct  59   HLTKPAITKAIKNLIAHGYVVATKDVNDKRSVNYQLSTEGMQLAAQHEASHRNLHHRIDH  118

Query  121  LGNKFTDEEQEVISKFLS  138
            FT  ++E I  FL+
Sbjct  119  TIATFTPAQRETIVAFLA  136
```

>ref|YP_501277.1| hypothetical protein SAOUHSC_02819 [Staphylococcus aureus subsp. aureus NCTC 8325]

  ref|YP_001333445.1| transcriptional regulator MarR family protein [Staphylococcus aureus subsp. aureus str. Newman]

  gb|ABD31821.1| conserved hypothetical protein [Staphylococcus aureus subsp. aureus NCTC 8325]

  dbj|BAF68683.1| transcriptional regulator MarR family protein [Staphylococcus aureus subsp. aureus str. Newman]
Length=152

  GENE ID: 3921258 SAOUHSC_02819 | hypothetical protein
[Staphylococcus aureus subsp. aureus NCTC 8325]

  Score = 62.8 bits (151), Expect = 8e-09, Method: Compositional matrix adjust.
  Identities = 40/112 (35%), Positives = 66/112 (58%), Gaps = 1/112 (0%)

```
Query  35   LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            L+ TQ HI+ L+     N K +++E L +S  A+TK++KKL  ++L+  S   ++R V
Sbjct  34   LSLTQFHIIELIDNNDKVNNKFLSEMLNVSKPAITKSIKKLLAKDLVVESHNEFNKREVN  93

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
            +SLT+K  ++ H   HEK++ Y+E+   F D+E VI +FL+    EE +
Sbjct  94   YSLTQKGKKLSYIHDELHEKSVKKYEEVLKVFDDDEMAVIIEFLNRSIEELK  145
```

>ref|ZP_03563431.1| MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus str. JKD6008]
  ref|ZP_03566444.1| MarR family transcriptional regulator [Staphylococcus aureus subsp. aureus str. JKD6009]
Length=154

  Score = 61.2 bits (147), Expect = 3e-08, Method: Compositional matrix adjust.
  Identities = 40/112 (35%), Positives = 65/112 (58%), Gaps = 1/112 (0%)

```
Query  35   LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            L+ TQ HI+ L+     N K +++E L +S  A+TK++KKL  ++L+  S   ++R V
Sbjct  36   LSLTQFHIIELIDNNDKVNNKFLSEMLNVSKPAITKSIKKLLAKDLVVESHNEFNKREVN  95

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
            SLT+K  ++ H   HEK++ Y+E+   F D+E VI +FL+    EE +
Sbjct  96   CSLTQKGKKLSYIHDELHEKSVKKYEEVLKVFDDDEMAVIIEFLNRSIEELK  147
```

>ref|YP_174450.1| MarR family transcriptional regulator [Bacillus clausii KSM-K16]

  dbj|BAD63489.1| MarR family transcriptional regulator [Bacillus clausii KSM-K16]
Length=153

  GENE ID: 3204362 ABC0950 | MarR family transcriptional regulator
[Bacillus clausii KSM-K16] (10 or fewer PubMed links)

  Score = 60.5 bits (145), Expect = 4e-08, Method: Compositional matrix adjust.
  Identities = 40/128 (31%), Positives = 73/128 (57%), Gaps = 3/128 (2%)

```
Query  18   AENKHEILLGKCESDV--KLTSTQEHILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKL  74
            A+ + + + G  E +    T TQ HI+ ++ EQ  +AE L +S  A+TKA+KKL
Sbjct  21   ADRRRKAMKGSQEESIVSDWTLTQLHIVAIVKEQERANNTMLAEHLNVSKPAITKAVKKL  80

Query  75   QEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVIS  134
            +Q++++ ++ ++++ V + LT+    +A  H+ HE+ + Y + +F  E EI
Sbjct  81   LDQQILEKTQQADNKKEVYYRLTKSGEMLAFIHSQLHEQARNRYMRIFAEFNSTELETII  140

Query  135  KFLSALTE  142
            +FL AL E
Sbjct  141  RFLHALAE  148
```

>ref|YP_080661.1| G transcriptional regulator YvnA [Bacillus licheniformis ATCC 14580]
 gb|AAU25023.1| G probable transcriptional regulator YvnA [Bacillus licheniformis ATCC 14580]
Length=157

 GENE ID: 3028745 yvnA | transcriptional regulator YvnA
[Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

 Score = 59.3 bits (142), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 37/105 (35%), Positives = 64/105 (60%), Gaps = 2/105 (1%)

```
Query  36   TSTQEHILMLLAEQIS--TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            T TQ HI+ L++E  +   NA +A KL+IS AAVTKA+  L +  +I+S +  N+ + +
Sbjct  47   TLTQLHIISLISESEADVNNAFLAAKLQISKAAVTKAVNVLTKHGMIESHKKPNNNKELY  106

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
            ++LT++    +A H   HE    Y EL ++F++ E + + +FL+
Sbjct  107  YTLTDEGKKLADIHDRMHEIAKQRYIELFDRFSESELQTVIRFLN  151
```


>ref|YP_254603.1| G hypothetical protein pSHaeC05 [Staphylococcus haemolyticus JCSC1435]
 dbj|BAE05997.1| G unnamed protein product [Staphylococcus haemolyticus JCSC1435]
Length=155

 GENE ID: 3431756 pSHaeC05 | hypothetical protein
[Staphylococcus haemolyticus JCSC1435] (10 or fewer PubMed links)

 Score = 59.3 bits (142), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 38/119 (31%), Positives = 69/119 (57%), Gaps = 1/119 (0%)

```
Query  28   KCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRAT  86
            K   D+ L+ TQ HI+ ++ +    N K +AE+L +S  AVTK++KKL  +EL+
Sbjct  29   KGNEDMDLSLTQFHIIEIIDKHEKVNNKFLAEELNVSKPAVTKSIKKLLSKELVVELNNE  88

Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
            +++R V ++LT++     ++  H   H+K +  Y+E+    F ++ E I +FL    +E +
Sbjct  89   SNKREVYYNLTKRGEKLSFIHDDLHKKAVKKYEEVLKVFDEKEMETIIEFLKRSVDELK  147
```


>ref|YP_093087.1| G YvnA [Bacillus licheniformis ATCC 14580]
 gb|AAU42394.1| G YvnA [Bacillus licheniformis DSM 13]
Length=160

 GENE ID: 3100261 yvnA | similar to proteins from B. subtilis
[Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

 Score = 59.3 bits (142), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 37/105 (35%), Positives = 64/105 (60%), Gaps = 2/105 (1%)

```
Query  36   TSTQEHILMLLAEQIS--TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            T TQ HI+ L++E  +   NA +A KL+IS AAVTKA+  L +  +I+S +  N+ + +
Sbjct  50   TLTQLHIISLISESEADVNNAFLAAKLQISKAAVTKAVNVLTKHGMIESHKKPNNNKELY  109

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
            ++LT++    +A H   HE    Y EL ++F++ E + + +FL+
Sbjct  110  YTLTDEGKKLADIHDRMHEIAKQRYIELFDRFSESELQTVIRFLN  154
```


>ref|ZP_00738634.1| Transcriptional regulator, MarR family [Bacillus thuringiensis serovar israelensis ATCC 35646]
 gb|EAO57135.1| Transcriptional regulator, MarR family [Bacillus thuringiensis serovar israelensis ATCC 35646]
Length=156

 Score = 55.8 bits (133), Expect = 9e-07, Method: Compositional matrix adjust.
 Identities = 32/106 (30%), Positives = 64/106 (60%), Gaps = 2/106 (1%)

```
Query  36   TSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            T TQ HI+ ++ E  Q   N   ++ +L IS A ++KA++ L + +++ + + T++++ +
Sbjct  46   TLTQLHIVSVIHESKQQMNNTLLSMELNISKATISKAIRVLIDNKILLTHQNTDNKKEIF  105

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSA  139
            ++LT+K + +A  H   H+      Y EL  +F D E ++++KFL A
Sbjct  106  YTLTDKGIQLAIVHKKLHKIAHERYSELFQQFNDSELQIVTKFLEA  151
```


>ref|ZP_02613091.1| transcriptional regulator, MarR family [Clostridium botulinum NCTC 2916]
 gb|EDT83321.1| transcriptional regulator, MarR family [Clostridium botulinum NCTC 2916]
Length=174

 Score = 54.3 bits (129), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

```
Query  30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN  87
            ++D+K  S  E H++ + +  +S N  IA +L ++   +K    KL  +EL+ + + N
Sbjct  58   DNDIKGISLSEFHVIECIGKNNMSNNIFIARELNMTKGGISKINSKLLSKDIIKADKIEN  117

Query  88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            D+R + +SLTEK + + K H   HEK        ++ + +  EE   I KFL L
Sbjct  118  DKREIYYSLTEKGIALFKLHEYLHEKEREKLMKILSNYKLEEITTILKFLEDL  170
```

>ref|YP_001253547.1| G MarR family transcriptional regulator [Clostridium botulinum
A str. ATCC 3502]
 ref|YP_001383390.1| G MarR family transcriptional regulator [Clostridium botulinum
A str. ATCC 19397]
 ref|YP_001386937.1| G MarR family transcriptional regulator [Clostridium botulinum
A str. Hall]
 emb|CAL82569.1| G MarR-family transcriptional regulator [Clostridium botulinum
A str. ATCC 3502]
 gb|ABS35317.1| G transcriptional regulator, MarR family [Clostridium botulinum
A str. ATCC 19397]
 gb|ABS36227.1| G transcriptional regulator, MarR family [Clostridium botulinum
A str. Hall]
Length=174

 GENE ID: 5185271 CBO1016 | MarR family transcriptional regulator
[Clostridium botulinum A str. ATCC 3502] (10 or fewer PubMed links)

 Score = 54.3 bits (129), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 63/113 (55%), Gaps = 2/113 (1%)

Query 30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN 87
            ++D+K S E H++ + + +S N IA++L   ++K   KL +++IK+ + N
Sbjct 58   DNDIKGISLSEFHVIECIGKNNMSNNIFIAKELNMTKGGISKINSKLLSKDIIKADKIEN 117

Query 88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
            D+R + +SLTEK + + K H   HEK   ++ + + EE   I KFL L
Sbjct 118 DKREIYYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKLEEITTILKFLEDL 170

>ref|YP_001780642.1| G MarR family transcriptional regulator [Clostridium botulinum
B1 str. Okra]
 gb|ACA44681.1| G transcriptional regulator, MarR family [Clostridium botulinum
B1 str. Okra]
Length=174

 GENE ID: 6149223 CLD_3550 | MarR family transcriptional regulator
[Clostridium botulinum B1 str. Okra] (10 or fewer PubMed links)

 Score = 54.3 bits (129), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 63/113 (55%), Gaps = 2/113 (1%)

Query 30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN 87
            ++D+K S E H++ + + +S N IA++L ++   ++K   KL +++IK+ + N
Sbjct 58   DNDIKGISLSEFHVIECIGKNNMSNNIFIAKELNMTKGGISKINSKLLSKDIIKADKIEN 117

Query 88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
            D+R + +SLTEK + + K H   HEK   ++ + + EE   I KFL L
Sbjct 118 DKREIYYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKLEEITTILKFLEDL 170

>ref|YP_001033131.1| G MarR family transcriptional regulator [Lactococcus lactis subsp.
cremoris MG1363]
 emb|CAL98430.1| G transcriptional regulator, MarR family [Lactococcus lactis subsp.
cremoris MG1363]
Length=295

 GENE ID: 4797387 rmaB | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 53.9 bits (128), Expect = 4e-06, Method: Compositional matrix adjust.
 Identities = 38/101 (37%), Positives = 54/101 (53%), Gaps = 3/101 (2%)

Query 42   ILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAV 101
            ++ L E TNA+IAE L I P++VT +K+L+E E++   + ND+RV   LTEK
Sbjct 47   LVELWNEDGLTNAEIAELLDIKPSSVTTQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGR 106

Query 102 PVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTE 142
              +   T H   T   GN TDEEQE ++ + L E
Sbjct 107 EAQETRDTMHNDISETI--FGN-LTDEEQEQLANLMEKLVE 144

>ref|ZP_02617530.1| transcriptional regulator, MarR family [Clostridium botulinum
Bf]
 gb|EDT85893.1| transcriptional regulator, MarR family [Clostridium botulinum
Bf]
Length=174

 Score = 53.9 bits (128), Expect = 4e-06, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

Query 30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN 87
            ++D+K S E H++ + + +S N IA+ L   ++K   KL +++IK+ + N
Sbjct 58   DNDIKGISLSEFHVIECIGKNNMSNNIFIAKDLNMTKGGISKINSKLLSKDIIKADKIEN 117

Query 88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL 140
            D+R + +SLTEK + + K H   HEK   ++ + + EE   I KFL L
Sbjct 118 DKREIYYSLTEKGIALFKLHEHIHEKEREKLMKILSNYKLEEITTILKFLEDL 170

>ref|YP_861960.1| G MarR family transcriptional regulator [Gramella forsetii KT0803]
 emb|CAL66893.1| G MarR family transcriptional regulator protein [Gramella forsetii

KT0803]
Length=158

GENE ID: 4650237 GFO_1928 | MarR family transcriptional regulator
[Gramella forsetii KT0803] (10 or fewer PubMed links)

Score = 53.9 bits (128), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 39/112 (34%), Positives = 65/112 (58%), Gaps = 8/112 (7%)

```
Query  1    MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQ--ISTNAKIAE    58
            + L NQI  + ++ +    ++  L KE   LT  Q +L++L E+  +S N KI E
Sbjct  7    LKLENQICFPIYSVSRLITKAYKPYLDKLE----LTYPQYLVLLVLWEEHKLSVN-KIGE   61

Query  59   KLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH          110
            KL ++    ++  LK++++ EL+K +R++NDER VL  LT+K +   KE A H
Sbjct  62   KLMLNTNTLSPLLKRMEKNELLKRNRSSNDERTVLVGLTDKGLSY-KEKAAH          112
```

>ref|NP_391388.1| **G** hypothetical protein BSU35080 [Bacillus subtilis subsp. subtilis
str. 168]
 ref|ZP_03593305.1| hypothetical protein Bsubs1_18986 [Bacillus subtilis subsp. subtilis
str. 168]
 ref|ZP_03597590.1| hypothetical protein BsubsN3_18902 [Bacillus subtilis subsp.
subtilis str. NCIB 3610]
 6 more sequence titles

 ref|ZP_03601994.1| hypothetical protein BsubsJ_18865 [Bacillus subtilis subsp. subtilis
str. JH642]
 ref|ZP_03606279.1| hypothetical protein BsubsS_19021 [Bacillus subtilis subsp. subtilis
str. SMY]
 sp|P40762.1|YVMB_BACSU RecName: Full=Uncharacterized HTH-type transcriptional regulator
yvmB
 emb|CAA85355.1| unnamed protein product [Bacillus subtilis]
 gb|AAC67278.1| YzhA [Bacillus subtilis]
 emb|CAB15513.1| **G** yvmB [Bacillus subtilis subsp. subtilis str. 168]
Length=169

GENE ID: 936625 yvmB | yvmB [Bacillus subtilis subsp. subtilis str. 168]
(10 or fewer PubMed links)

Score = 53.5 bits (127), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 36/91 (39%), Positives = 53/91 (58%), Gaps = 2/91 (2%)

```
Query  52    TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEH-ATH    110
             NA IA K+ +S A VTK   KL ++E I S + T++++ V + LT K  +   H  H
Sbjct  63    NNAGIARKMNLSKANVTKISTKLIKEEFINSYQLTDNKKEVYFKLTRKGRRIFDLHEKLH    122

Query  111   HEKTLSTYQELGNKFTDEEQEVISKFLSALT     141
             +K L+ YQ L + F+ EEQ+ + KFL  LT
Sbjct  123   KKKELAFYQFL-DSFSQEEQKAVLKFLEQLT     152
```

>ref|ZP_02994615.1| hypothetical protein CLOSPO_01734 [Clostridium sporogenes ATCC
15579]
 gb|EDU38872.1| hypothetical protein CLOSPO_01734 [Clostridium sporogenes ATCC
15579]
Length=174

Score = 53.5 bits (127), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 34/113 (30%), Positives = 63/113 (55%), Gaps = 2/113 (1%)

```
Query  30    ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN    87
             ++D+K  S  E H++  + +  +S N  IA++L    KK   KL ++  N
Sbjct  58    DNDIKEISLSEFHVIECIGKNNMSNNIFIAKELNMTKGGISKINSKLLSKDIIKADKIEN    117

Query  88    DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL         140
             D+R + +SLTEK + + K H  H+K      ++ + +  EE    I KFL  L
Sbjct  118   DKREIYYSLTEKGIVLFKLHEYLHKKEQEKLMKILSNYKQEEITTILKFLDDL         170
```

>ref|ZP_01994138.1| hypothetical protein DORLON_00120 [Dorea longicatena DSM 13814]
 gb|EDM64274.1| hypothetical protein DORLON_00120 [Dorea longicatena DSM 13814]
Length=153

Score = 53.1 bits (126), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 36/111 (32%), Positives = 55/111 (49%), Gaps = 4/111 (3%)

```
Query  35    LTSTQEHILMLLAEQISTN-AKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL    93
             LT+  H++ +    N + IA KL I+  ++T A+ L  +  ++ R+  D RVVL
Sbjct  37    LTNNDMHVIEAVGLGDGNNMSSIARKLNITVGSLTTAMNSLVNKRYVERHRSEEDRRVVL    96

Query  94    WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF          144
             LTEK V    H  +H +    Q + +K  D E  V+ K L AL+E F
Sbjct  97    VKLTEKGVKAYHHHEDYHRQMT---QAILDKLDDTELPVLVKTLDALSEFF          144
```

>ref|ZP_03294064.1| hypothetical protein CLOHIR_02015 [Clostridium hiranonis DSM
13275]
 gb|EEA84316.1| hypothetical protein CLOHIR_02015 [Clostridium hiranonis DSM
13275]
Length=166

Score = 53.1 bits (126), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 37/131 (28%), Positives = 68/131 (51%), Gaps = 6/131 (4%)

```
Query  13    TIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTN-AKIAEKLKISPAAVTKAL    71
```

```
                   T  +F     HE    G+       K+    + H++   + E      N ++++E+L I+   AV++ L
Sbjct   20   TYYKFLSTPHEYYPGE-----KMHMREVHVITEIGEGGLDNISELSERLNITKGAVSQYL   74

Query   72   KKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE   131
             KKL+++ I+  + + D+R     LTEK   + K H  + E+  +         N+FT+EE E
Sbjct   75   KKLEKKGFIERVQESEDKRQYSVRLTEKGKELDKIHTKYDEEQYAKACPFFNEFTEEELE   134

Query  132   VISKFLSALTE   142
             +I +F  +   E
Sbjct  135   LICRFEARFAE   145
```

>ref|**ZP_02211326.1**| hypothetical protein CLOBAR_00939 [Clostridium bartlettii DSM 16795]
  gb|**EDQ97187.1**| hypothetical protein CLOBAR_00939 [Clostridium bartlettii DSM 16795]
Length=150

 Score = 52.4 bits (124), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 33/94 (35%), Positives = 50/94 (53%), Gaps = 3/94 (3%)

```
Query   52   TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHH   111
             T +IA L+I+   +T A+ +L ++    + SR   D RVVL SLTEK    K HA  H
Sbjct   53   TMGEIAHDLRITVGTLTSAINRLIKKGYAERSRTEEDRRVVLVSLTEKGKHAYKIHADFH   112

Query  112   EKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ   145
             ++ +   Q   N + DEEQEV+   +    F+
Sbjct  113   KEMV---QATLNSYNDEEQEVLCDVIEKINIFFE   143
```

>ref|**YP_001390364.1**| 🄖 MarR family transcriptional regulator [Clostridium botulinum F str. Langeland]
  gb|**ABS39442.1**| 🄖 transcriptional regulator, MarR family [Clostridium botulinum F str. Langeland]
Length=174

 GENE ID: 5405444 CLI_1098 | MarR family transcriptional regulator [Clostridium botulinum F str. Langeland]

 Score = 52.4 bits (124), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 34/113 (30%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

```
Query   30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN   87
             ++D+K  S  E H++  + +  +S N  IA++L ++    ++K   KL +++IK+ +  N
Sbjct   58   DNDIKGISLSEFHVIECIGKNNMSNNIFIAKELNMTKGGISKINSKLLSKDIIKADKIEN   117

Query   88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL   140
             D+R + +SLTEK + + K H     HEK        ++ + +  EE   I  FL   L
Sbjct  118   DKREIYYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKLEEITTILNFLEDL   170
```

>ref|**YP_001786407.1**| 🄖 MarR family transcriptional regulator [Clostridium botulinum A3 str. Loch Maree]
  gb|**ACA55750.1**| 🄖 transcriptional regulator, MarR family [Clostridium botulinum A3 str. Loch Maree]
Length=174

 GENE ID: 6154364 CLK_0459 | MarR family transcriptional regulator [Clostridium botulinum A3 str. Loch Maree] (10 or fewer PubMed links)

 Score = 51.6 bits (122), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 33/113 (29%), Positives = 62/113 (54%), Gaps = 2/113 (1%)

```
Query   30   ESDVKLTSTQE-HILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATN   87
             ++D+K  S  E H++  + +  +S N  IA++L ++    + N   IA++L ++    ++K   + N
Sbjct   58   DNDIKGISLSEFHVIECIGKNNMPNNIFIAKELNMTKGGISKINSKLLLKDIIRADKIEN   117

Query   88   DERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL   140
             D+R + +SLTEK + + K H     HEK        ++ + +  EE   I KFL   L
Sbjct  118   DKREIYYSLTEKGIALFKLHEHLHEKEREKLMKILSNYKQEEITTILKFLEDL   170
```

>ref|**YP_808725.1**| 🄖 transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
  gb|**ABJ72303.1**| 🄖 Transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=292

 GENE ID: 4432217 LACR_0742 | transcriptional regulator [Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 51.2 bits (121), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

```
Query   52   TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHH   111
             TNA+IAE L I P++VT +K+L+E E++  +  ND+RV    LTEK    +   T H
Sbjct   57   TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGREAQETRDTMH   116

Query  112   EKTLSTYQELGNKFTDEEQEVISKFLSALTE   142
                 T     GN  TDEEQ+ ++  +    L E
Sbjct  117   NDISETI--FGN-LTDEEQKQLANLMEKLVE   144
```

>ref|YP_001698248.1| ⒢ MarR family transcriptional regulator [Lysinibacillus sphaericus C3-41]
  gb|ACA40118.1| ⒢ transcriptional regulator, MarR family [Lysinibacillus sphaericus C3-41]
Length=162

 GENE ID: 6022244 Bsph_2567 | MarR family transcriptional regulator
(Lysinibacillus sphaericus C3-41] (10 or fewer PubMed links)

 Score = 51.2 bits (121), Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 36/111 (32%), Positives = 60/111 (54%), Gaps = 1/111 (0%)

```
Query  36   TSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLW   94
            T TQ HI+  +  Q S N   ++E L +S  A+TKA+KK+ E+ +I  +R   +++ V +
Sbjct  44   TLTQLHIVSAIKAQGSANNTFLSETLNVSKPAITKAIKKMLEKNVIVETRQEANQKEVHY   103

Query  95   SLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ   145
            LT      ++  H   HEK  + Y  L + F  +E E I  FL  +T++ +
Sbjct  104  LLTAFGKQLSSIHEQLHEKARNRYLRLLDSFNTDELETIVTFLEMITDKLK   154
```


>ref|NP_266864.1| ⒢ transcription regulator [Lactococcus lactis subsp. lactis Il1403]
  gb|AAK04806.1|AE006304_6 ⒢ transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Length=291

 GENE ID: 1114333 rmaB | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 51.2 bits (121), Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

```
Query  52   TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHH   111
            TNA+IAE L I P++VT  +K+L+E E++  +  ND+RV    LT+K   +    T H
Sbjct  57   TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVSRIFLTDKGREAQETRDTMH   116

Query  112  EKTLSTYQELGNKFTDEEQEVISKFLSALTE   142
             T   GN TDEEQE ++ +  L E
Sbjct  117  NDISETI--FGN-LTDEEQEQLAFLMEKLVE   144
```


>ref|ZP_01723095.1| transcriptional regulator, MarR family protein [Bacillus sp. B14905]
  gb|EAZ86562.1| transcriptional regulator, MarR family protein [Bacillus sp. B14905]
Length=162

 Score = 50.4 bits (119), Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 35/111 (31%), Positives = 60/111 (54%), Gaps = 1/111 (0%)

```
Query  36   TSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLW   94
            T TQ HI+  +  Q S N   ++E L +S  A+TKA+KK+ E+ +I  +R   +++ + +
Sbjct  44   TLTQLHIVSAIKAQGSANNTFLSETLNVSKPAITKAIKKMLEKNVIVETRQEANQKEIHY   103

Query  95   SLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ   145
            LT      ++  H   HEK  + Y  L + F  +E E I  FL  +T++ +
Sbjct  104  LLTAFGKQLSSIHEQLHEKARNRYLRLLDSFNTDELETIITFLEMITDKLK   154
```


>ref|YP_808147.1| ⒢ transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
  gb|ABJ71725.1| ⒢ Transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=169

 GENE ID: 4432499 LACR_0099 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 50.4 bits (119), Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 27/98 (27%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query  41   HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA   100
            HIL  L ++  T  ++A KL ++    VT+A++ L + + + +A ND++ + + +T K
Sbjct  53   HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG   112

Query  101  VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS   138
            + VA  H   H+        ++ +K+ + E+ +I  FLS
Sbjct  113  LKVASIHDKMHKIMDLKLGQIFDKYNENEKSIILNFLS   150
```


>ref|NP_786298.1| ⒢ transcription regulator [Lactobacillus plantarum WCFS1]
  emb|CAD65154.1| ⒢ transcription regulator [Lactobacillus plantarum WCFS1]
Length=178

 GENE ID: 1063436 lp_2967 | transcription regulator
[Lactobacillus plantarum WCFS1] (10 or fewer PubMed links)

 Score = 50.1 bits (118), Expect = 6e-05, Method: Compositional matrix adjust.
 Identities = 33/104 (31%), Positives = 57/104 (54%), Gaps = 5/104 (4%)

```
Query  39   QEHILMLLAEQIS--TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSL   96
            Q  IL +LA+  +   TNA+IAE L I P++V+  L +L++  LI+  + +D+RVV  L
Sbjct  43   QMGILRVLADAPAGLTNAEIAEILDIRPSSVSATLNRLEDGGLIEREPSAHDKRVVIVRL   102
```

```
Query   97   TEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL   140
             +++   +A   A   + T     +L    TD+E+   +   L L
Sbjct  103   SDRGREMADHRA---QGTSDLADQLFGNLTDDERNQLQHLLDKL   143
```

>ref|YP_757477.1| **G** MarR family transcriptional regulator [Maricaulis maris MCS10]
  gb|ABI66539.1| **G** transcriptional regulator, MarR family [Maricaulis maris MCS10]
Length=143

  GENE ID: 4285355 **Mmar10_2247** | MarR family transcriptional regulator
[Maricaulis maris MCS10]

  Score = 50.1 bits (118), Expect = 6e-05, Method: Compositional matrix adjust.
  Identities = 39/146 (26%), Positives = 75/146 (51%), Gaps = 5/146 (3%)

```
Query    1   MSLANQIDQFLGTIMQFAENK-HEILLGKCESDVKLTSTQEHILMLLAEQISTN-AKIAE    58
             M+ A  +D+ L  +++ A  K +   + +S   +TS Q  +L LLA +       I E
Sbjct    1   MARARAVDRRLFLLLEIAARKLNRDADARLKSVAGVTSAQAAVLFLLARRGERRMGDIGE    60

Query   59   KLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTY   118
             L + P AVT  + +++    L+    + +D+R  + SLTEK   +  + A H  + L+T
Sbjct   61   MLSLHPPAVTGLVNRMEALGLVTKKTSPSDKRSAIVSLTEKGRALG-DTADHILRDLNT-   118

Query  119   QELGNKFTDEEQEVISKFLSALTEEF   144
             EL N+  +E+ +++ + L+ +  +F
Sbjct  119   -ELENRLGEEDADMLHRVLTRIAVDF   143
```

>ref|NP_391385.1| **G** hypothetical protein BSU35050 [Bacillus subtilis subsp. subtilis
str. 168]
  ref|ZP_03593302.1| hypothetical protein Bsubs1_18971 [Bacillus subtilis subsp. subtilis
str. 168]
  ref|ZP_03597587.1| hypothetical protein BsubsN3_18887 [Bacillus subtilis subsp.
subtilis str. NCIB 3610]
  ref|ZP_03601991.1| hypothetical protein BsubsJ_18850 [Bacillus subtilis subsp. subtilis
str. JH642]
  ref|ZP_03606276.1| hypothetical protein BsubsS_19006 [Bacillus subtilis subsp. subtilis
str. SMY]
  sp|O34692.1|**YVNA_BACSU** RecName: Full=Uncharacterized HTH-type transcriptional regulator
yvnA
  gb|AAC67281.1| YvnA [Bacillus subtilis]
  emb|CAB15510.1| **G** yvnA [Bacillus subtilis subsp. subtilis str. 168]
Length=157

  GENE ID: 936639 **vvnA** | vvnA [Bacillus subtilis subsp. subtilis str. 168]
(10 or fewer PubMed links)

  Score = 50.1 bits (118), Expect = 6e-05, Method: Compositional matrix adjust.
  Identities = 30/104 (28%), Positives = 59/104 (56%), Gaps = 1/104 (0%)

```
Query   36   TSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLW    94
             T TQ HI+   +    Q  N+ +A +L IS AAV+KA+  L  +I   ++   +++ + +
Sbjct   48   TLTQLHIVSCIHTSQNVNNSFLASRLHISKAAVSKAVHALLKHNIITVTKKPGNKKEIFY   107

Query   95   SLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS   138
             +LT+    +A  H   HEK    Y++L N+F+  ++ + ++ F +
Sbjct  108   TLTDSGRKLAALHEQLHEKAKEQYKQLFNEFSIDDLKTVTAFFN   151
```

>ref|NP_111681.1| **G** transcription regulator (SlyA-related) [Thermoplasma volcanium
GSS1]
  dbj|BAB60329.1| **G** hypothetical protein [Thermoplasma volcanium GSS1]
Length=143

  GENE ID: 1441302 **TVN1162** | transcription regulator (SlyA-related)
[Thermoplasma volcanium GSS1] (10 or fewer PubMed links)

  Score = 49.7 bits (117), Expect = 7e-05, Method: Compositional matrix adjust.
  Identities = 30/81 (37%), Positives = 45/81 (55%), Gaps = 0/81 (0%)

```
Query   26   LGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRA    85
             +G+  S +       + IL LL+E  ST  K+AE    ++PA +T  L +++  Q LI  SR+
Sbjct   27   MGESLSHISAKPIEVRILYLLSEDESTVNKLAELTDVTPAWITGTLDEMESQGLIVRSRS    86

Query   86   TNDERVVLWSLTEKAVPVAKE   106
             D RVV    +TEK + V  E
Sbjct   87   GEDRRVVNVHITEKGIEVLNE   107
```

>ref|NP_419215.1| **G** MarR family transcriptional regulator [Caulobacter crescentus
CB15]
  ref|YP_002515775.1| **G** transcriptional regulator, MarR family [Caulobacter crescentus
NA1000]
  gb|AAK22383.1| **G** transcriptional regulator, MarR family [Caulobacter crescentus
CB15]
  gb|ACL93867.1| **G** transcriptional regulator, MarR family [Caulobacter crescentus
NA1000]
Length=147

  GENE ID: 942105 **CC_0396** | MarR family transcriptional regulator
[Caulobacter crescentus CB15] (10 or fewer PubMed links)

```
Score = 49.3 bits (116),  Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 32/119 (26%), Positives = 63/119 (52%), Gaps = 4/119 (3%)

Query  27  GKCESDVKLTSTQEHILMLLAEQIST-NAKIAEKLKISPAAVTKALKKLQEQELIKSSRA  85
               G+  ++  LT+ Q  +L   L E+       + A+ L ++P+A+T  + ++   EL++
Sbjct  26  GRMAAEGGLTAAQSGVLFFLGERDGALIGEAADALDLAPSAMTGLIDRMARAELVERRAD  85

Query  86  TNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
               D R +   LT+K   A++ A    + ++   +L    FTDEE  V+S++L++L  +F
Sbjct  86  AKDGRAMHLHLTDKGR-AARDTAKAGLRGVNA--QLTEGFTDEEISVVSRWLASLQTKF  141
```


>ref|YP_001031482.1| 🅖 MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]

emb|CAL96727.1| 🅖 transcriptional regulator, MarR family [Lactococcus lactis subsp. cremoris MG1363]
Length=172

GENE ID: 4798609 rmaD | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

```
Score = 49.3 bits (116),  Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

Query  41  HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA  100
           HIL  L ++  T  ++A KL ++    VT+A++ L + + + +A ND++ + + +T K
Sbjct  56  HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG  115

Query  101 VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
           + VA  H   H+         ++ +K+ + ++ +I  FLS
Sbjct  116 LKVASIHDKMHKIMDLKLGQIFDKYNENDKSIILNFLS  153
```


>ref|NP_603578.1| 🅖 MarR family transcriptional regulator [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]

gb|AAL94877.1| 🅖 Transcriptional regulator, MarR family [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]
Length=225

GENE ID: 991648 FN0681 | MarR family transcriptional regulator
[Fusobacterium nucleatum subsp. nucleatum ATCC 25586] (10 or fewer PubMed links)

```
Score = 48.9 bits (115),  Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 29/88 (32%), Positives = 50/88 (56%), Gaps = 3/88 (3%)

Query  35  LTSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVV  92
           LT T+ HI+  + E  Q++ N ++A+K+ I+     T A+ KL ++  I  +R+T D R V
Sbjct  34  LTHTELHIIESIGENTQLTMN-ELADKIGITMGTATVAISKLSDKGYIDRARSTTDRRKV  92

Query  93  LWSLTEKAVPVAKEHATHHEKTLSTYQE  120
            SLT+K V     H  +H+  +++  E
Sbjct  93  FVSLTKKGVDALTYHNNYHKMIMASITE  120
```


>ref|YP_138915.1| 🅖 MarR family transcriptional regulator [Streptococcus thermophilus LMG 18311]

gb|AAV60100.1| 🅖 transcriptional regulator, MarR family [Streptococcus thermophilus LMG 18311]
Length=144

GENE ID: 3164787 stu0381 | MarR family transcriptional regulator
[Streptococcus thermophilus LMG 18311] (10 or fewer PubMed links)

```
Score = 48.9 bits (115),  Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 31/90 (34%), Positives = 51/90 (56%), Gaps = 3/90 (3%)

Query  51  STNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH  110
           +T + +A +L ++    VT +L KL+++  I  +R++ D RVV   SL++K    V + H
Sbjct  50  TTPSAVARELMLTLGTVTTSLNKLEKKGYIIRTRSSVDRRVVHLSLSKKGRLVYRLHRGF  109

Query  111 HEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
           H+  + T  E    F DEE +V+SK L  L
Sbjct  110 HKSMVKTITE---GFNDEELKVMSKGLENL  136
```


>ref|YP_002165566.1| 🅖 possible MarR family transcriptional regulator [Fusobacterium nucleatum subsp. polymorphum ATCC 10953]

gb|EDK89119.1| 🅖 possible MarR family transcriptional regulator [Fusobacterium nucleatum subsp. polymorphum ATCC 10953]
Length=225

GENE ID: 6818656 FNP_1336 | possible MarR family transcriptional regulator
[Fusobacterium nucleatum subsp. polymorphum ATCC 10953]

```
Score = 48.9 bits (115),  Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 29/88 (32%), Positives = 50/88 (56%), Gaps = 3/88 (3%)

Query  35  LTSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVV  92
           LT T+ HI+  + E  Q++ N ++A+K+ I+     T A+ KL ++  I  +R+T D R V
Sbjct  34  LTHTELHIIESIGENTQLTMN-ELADKIGITMGTATVAISKLSDKGYIDRARSTTDRRKV  92

Query  93  LWSLTEKAVPVAKEHATHHEKTLSTYQE  120
            SLT+K V     H  +H+  +++  E
```

Sbjct   93   FVSLTKKGVDALTYHNNYHKMIMASLTE   120·

>ref|ZP_00144611.1| Transcriptional regulator, MarR family [Fusobacterium nucleatum subsp. vincentii ATCC 49256]
 gb|EAA23791.1| Transcriptional regulator, MarR family [Fusobacterium nucleatum subsp. vincentii ATCC 49256]
Length=225

  Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
  Identities = 29/88 (32%), Positives = 50/88 (56%), Gaps = 3/88 (3%)

Query   35   LTSTQEHILMLLAE--QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVV   92
             LT T+ HI+ + E Q++ N ++A+K+ I+   T A+ KL ++ I +R+T D R V
Sbjct   34   LTHTELHIIESIGENTQLTMN-ELADKIGITMGTATVAISKLSDKGYIDRARSTTDRRKV   92

Query   93   LWSLTEKAVPVAKEHATHHEKTLSTYQE   120
             SLT+K V   H +H+ +++ E
Sbjct   93   FVSLTKKGVDALTYHNNYHKMIMASITE   120

>ref|YP_819912.1| G MarR family transcriptional regulator [Streptococcus thermophilus LMD-9]
 gb|ABJ65716.1| G transcriptional regulator, MarR family [Streptococcus thermophilus LMD-9]
Length=144

  GENE ID: 4437359 STER_0428 | MarR family transcriptional regulator
[Streptococcus thermophilus LMD-9] (10 or fewer PubMed links)

  Score = 48.9 bits (115), Expect = 1e-04, Method: Compositional matrix adjust.
  Identities = 31/90 (34%), Positives = 51/90 (56%), Gaps = 3/90 (3%)

Query   51   STNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH   110
             +T + +A +L ++   VT +L KL+++ I +R++ D RVV SL++K   V + H
Sbjct   50   TTPSAVARELMLTLGTVTTSLNKLEKKGYIIRTRSSVDRRVVHLSLSKKGRLVYRLHRAF   109

Query   111 HEKTLSTYQELGNKFTDEEQEVISKFLSAL   140
             H+   T E   F DEE +V+SK L L
Sbjct   110 HKSMVKTITE---GFNDEELKVMSKGLENL   136

>ref|YP_079349.1| G transcriptional regulator YvmB [Bacillus licheniformis ATCC 14580]
 gb|AAU23711.1| G possible transcriptional regulator YvmB [Bacillus licheniformis ATCC 14580]
Length=161

  GENE ID: 3031484 yvmB | transcriptional regulator YvmB
[Bacillus licheniformis ATCC 14580] (10 or fewer PubMed links)

  Score = 48.5 bits (114), Expect = 2e-04, Method: Compositional matrix adjust.
  Identities = 35/117 (29%), Positives = 59/117 (50%), Gaps = 4/117 (3%)

Query   29   CESDVKL---TSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSR   84
             ESDVK   T H++ + ++   N IA+K+ +S A +TK   KL++++ I +
Sbjct   36   AESDVKRLPGNMTTIHVISCIGHDEPINNTGIAKKMNLSKANITKISSKLLKEGLIKRFQ   95

Query   85   ATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALT   141
             T++++ + + LT   V + H H++ +   + F+ EQ I KFL LT
Sbjct   96   LTDNKKEIYFRLTPSGKQVFELHEKLHQQKADQFSRFLDSFSTAEQGAILKFLQGLT   152

>ref|ZP_01219563.1| putative transcriptional regulator, MarR family protein [Photobacterium profundum 3TCK]
 gb|EAS43796.1| putative transcriptional regulator, MarR family protein [Photobacterium profundum 3TCK]
Length=138

  Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
  Identities = 39/143 (27%), Positives = 73/143 (51%), Gaps = 13/143 (9%)

Query   7   IDQFLGTIMQFAEN----KHEILLGKCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLK   61
             I+Q   TI++F E   + ++ GK   + Q HI+ +L   + K +A+K+
Sbjct   4   IEQLNHTIIEFYEKLSSWEQSVVRGKG-----FSLPQVHIVEILGAHGAMRMKELADKIG   58

Query   62   ISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQEL   121
             ++   +T + K+ + ELI+   +D R +L LTEK V + +EH   H   LS Q++
Sbjct   59   VTTGTLTVQVDKMVQAELIQRRPHESDRRSILVDLTEKGVEMYQEHDHLH---LSLTQDI   115

Query   122 GNKFTDEEQEVISKFLSALTEEF   144
             +   D E++ + +L+ + +EF
Sbjct   116 TAQLDDVERKNLLMYLTKMNQEF   138

>ref|YP_091766.1| G YvmB [Bacillus licheniformis ATCC 14580]
 gb|AAU41073.1| G YvmB [Bacillus licheniformis DSM 13]
Length=163

  GENE ID: 3097946 yvmB | YvmB [Bacillus licheniformis ATCC 14580]
(10 or fewer PubMed links)

  Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
  Identities = 35/117 (29%), Positives = 59/117 (50%), Gaps = 4/117 (3%)

```
Query  29   CESDVKL---TSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSR  84
            ESDVK    T  H++  +   ++     N  IA+K+ +S A +TK   KL ++ LIK  +
Sbjct  38   AESDVKRLPGNMTTIHVISCIGHDEPINNTGIAKKMNLSKANITKISSKLLKEGLIKRFQ  97

Query  85   ATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALT  141
            T++++ + + LT     V + H  H++    +    + F+  EQ  I KFL  LT
Sbjct  98   LTDNKKEIYFRLTPSGKQVFELHEKLHQQKADQFSRFLDSFSTAEQGAILKFLQGLT  154
```

>**ref|YP_129221.1|** [G] MarR family transcriptional regulator [Photobacterium profundum SS9]

  emb|CAG19419.1| [G] putative transcriptional regulator, MarR family [Photobacterium profundum SS9]
Length=138

 GENE ID: 3122954 PBPRA1008 | MarR family transcriptional regulator
[Photobacterium profundum SS9] (10 or fewer PubMed links)

 Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 39/143 (27%), Positives = 73/143 (51%), Gaps = 13/143 (9%)

```
Query  7    IDQFLGTIMQFAEN----KHEILLGKCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLK  61
            I+Q  TI++F E      +  ++ GK      +  Q HI+ +L    +    K   K+A+K+
Sbjct  4    IEQLNHTIIEFYEKLSSWEQSVVRGKG-----FSLPQIHIVEILGAHGAMRMKELADKIG  58

Query  62   ISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQEL  121
            ++   +T  + K+  ELI+       +D R +L  LTE+ V +  +EH    H    LS  Q++
Sbjct  59   VTTGTLTVQVDKMVQAELIQRRPHESDRRSILVDLTEQGVEMYQEHDHLH---LSLTQDI  115

Query  122  GNKFTDEEQEVISKFLSALTEEF  144
               K  D E++  +  +L+ +  +EF
Sbjct  116  TAKLDDTERKNLLMYLTKMNQEF  138
```

>**ref|ZP_00990845.1|** hypothetical transcriptional regulator, MarR family [Vibrio splendidus 12B01]
 gb|EAP94213.1| hypothetical transcriptional regulator, MarR family [Vibrio splendidus 12B01]
Length=301

 Score = 48.1 bits (113), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 35/117 (29%), Positives = 62/117 (52%), Gaps = 1/117 (0%)

```
Query  25   LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSR  84
            +L K    D+ L   Q H L+ L +Q  T  ++A+KL I  +  ++A+  L  + LI++S
Sbjct  19   MLDKDCGDIALPPIQAHTLIELEQQPLTVNQLADKLNIDKSNASRAVNNLAKNSLIQTSP  78

Query  85   ATNDERVVLWSLTEKAV-PVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            ND+R V+ S+TE+ +  +A+ H+ ++    S  +  L    T +    I  +L AL
Sbjct  79   HPNDKRSVVASVTEQGIKTLAQLHSQQNQFYDSVLERLTEAETQQVSGGIKHYLKAL  135
```

>**ref|YP_001319891.1|** [G] MarR family transcriptional regulator [Alkaliphilus metalliredigens QYMF]

 gb|ABR48232.1| [G] transcriptional regulator, MarR family [Alkaliphilus metalliredigens QYMF]
Length=143

 GENE ID: 5312143 Amet_2072 | MarR family transcriptional regulator
[Alkaliphilus metalliredigens QYMF]

 Score = 47.8 bits (112), Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 27/67 (40%), Positives = 42/67 (62%), Gaps = 1/67 (1%)

```
Query  35   LTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL  93
            +T TQ   L++L E+    AK + EKL +     +T  LKKL+ +ELI    R+T DER+++
Sbjct  37   ITYTQYITLLVLWEKPKITAKELGEKLYLDSGTLTPLLKKLESKELITRKRSTKDERIMI  96

Query  94   WSLTEKA  100
            +LT+K
Sbjct  97   VTLTDKG  103
```

>**ref|YP_001838202.1|** [G] MarR family transcriptional regulator [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)']

 gb|ABZ96926.1| [G] Putative transcriptional regulator, MarR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)']
Length=133

 GENE ID: 6222463 LEPBI_I0798 | MarR family transcriptional regulator
[Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)']
(10 or fewer PubMed links)

 Score = 47.8 bits (112), Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 26/71 (36%), Positives = 45/71 (63%), Gaps = 1/71 (1%)

```
Query  31   SDVKLTSTQEHILMLLAEQ-ISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDE  89
            +D+  LT  Q  ++++++ E+ IST +KI +KL++      +T  LK+L++ EL+    R  NDE
Sbjct  26   ADLGLTYPQYLVMLVMWEEKISTVSKIGDKLQLDSGTLTPLLKRLEQMELLDRMRNPNDE  85

Query  90   RVVLWSLTEKA  100
            R V   L++K
Sbjct  86   RSVNIVLSKKG  96
```

>ref|YP_108512.1| [G] putative transcriptional regulatory protein [Burkholderia pseudomallei K96243]

ref|YP_102754.1| [G] MarR family transcriptional regulator [Burkholderia mallei ATCC 23344]
ref|ZP_00438156.1| COG1846: Transcriptional regulators [Burkholderia mallei GB8 horse 4]
46 more sequence titles

ref|YP_333321.1| [G] MarR family transcriptional regulator [Burkholderia pseudomallei 1710b]

ref|YP_992831.1| [G] MarR family transcriptional regulator [Burkholderia mallei SAVP1]

ref|YP_001026174.1| [G] MarR family transcriptional regulator [Burkholderia mallei NCTC 10229]

ref|YP_001058785.1| [G] MarR family transcriptional regulator [Burkholderia pseudomallei 668]

ref|YP_001080556.1| [G] MarR family transcriptional regulator [Burkholderia mallei NCTC 10247]

ref|YP_001066038.1| [G] MarR family transcriptional regulator [Burkholderia pseudomallei 1106a]
ref|ZP_01769009.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 305]
ref|ZP_02102319.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 1106b]
ref|ZP_02109049.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 1710a]
ref|ZP_02266811.1| transcriptional regulator, MarR family protein [Burkholderia mallei PRL-20]
ref|ZP_02403045.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei DM98]
ref|ZP_02411585.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 14]
ref|ZP_02447714.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 91]
ref|ZP_02455880.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 9]
ref|ZP_02471448.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei B7210]
ref|ZP_02481920.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 7894]
ref|ZP_02490126.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei NCTC 13177]
ref|ZP_02498250.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei 112]
ref|ZP_02506273.1| transcriptional regulator, MarR family protein [Burkholderia pseudomallei BCC215]

ref|YP_002009903.1| [G] transcriptional regulator, MarR family [Burkholderia mallei ATCC 10399]

ref|YP_002036065.1| [G] transcriptional regulator, MarR family [Burkholderia pseudomallei 1655]

ref|YP_002022669.1| [G] transcriptional regulator, MarR family [Burkholderia pseudomallei Pasteur 52237]

ref|YP_002050288.1| [G] transcriptional regulator, MarR family [Burkholderia pseudomallei S13]

ref|YP_002060819.1| [G] transcriptional regulator, MarR family [Burkholderia mallei FMH]
ref|YP_002064980.1| [G] transcriptional regulator, MarR family [Burkholderia mallei JHU]
ref|YP_002106328.1| [G] transcriptional regulator, MarR family [Burkholderia pseudomallei 406e]

ref|YP_002110157.1| [G] transcriptional regulator, MarR family [Burkholderia mallei 2002721280]
ref|ZP_03454874.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 576]

emb|CAH35912.1| [G] putative transcriptional regulatory protein [Burkholderia pseudomallei K96243]

gb|AAU48847.1| [G] transcriptional regulator, MarR family [Burkholderia mallei ATCC 23344]

gb|ABA50381.1| [G] transcriptional regulator, MarR family [Burkholderia pseudomallei 1710b]

gb|ABM52457.1| [G] transcriptional regulator, MarR family [Burkholderia mallei SAVP1]
gb|ABN02741.1| [G] transcriptional regulator, MarR family [Burkholderia mallei NCTC 10229]

gb|ABN82036.1| [G] transcriptional regulator, MarR family [Burkholderia pseudomallei 668]

gb|ABN89050.1| [G] transcriptional regulator, MarR family [Burkholderia pseudomallei 1106a]

gb|ABO05799.1| [G] transcriptional regulator, MarR family [Burkholderia mallei NCTC 10247]
gb|EBA46431.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 305]

gb|EDK56373.1| [G] transcriptional regulator, MarR family [Burkholderia mallei FMH]
gb|EDK60534.1| [G] transcriptional regulator, MarR family [Burkholderia mallei JHU]
gb|EDK85546.1| [G] transcriptional regulator, MarR family [Burkholderia mallei 2002721280]
gb|EDO84870.1| [G] transcriptional regulator, MarR family [Burkholderia pseudomallei

406e]
gb|EDO91962.1| transcriptional regulator, MarR family [Burkholderia pseudomallei Pasteur 52237]
gb|EDP89187.1| transcriptional regulator, MarR family [Burkholderia mallei ATCC 10399]
gb|EDS86631.1| transcriptional regulator, MarR family [Burkholderia pseudomallei S13]
gb|EDU07559.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 1655]
gb|EEC33252.1| transcriptional regulator, MarR family [Burkholderia pseudomallei 576]
Length=165

GENE ID: 3092472 BPSL1912 | putative transcriptional regulatory protein [Burkholderia pseudomallei K96243] (10 or fewer PubMed links)

 Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 33/126 (26%), Positives = 69/126 (54%), Gaps = 5/126 (3%)

```
Query  6    QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS  63
            QI+ +G +M   ++    ++ + ++++ +T TQ +L +LA + ST A++A + I
Sbjct  17   QINDSVGYLMSRVKSLMTNMVTQRTQTELGITGTQATMLFMLAVGKCSTAAELAREYGID  76

Query  64   PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN  123
            +A+T+ L +++++ L++  R++ D RVV   LT++   + K        L    E+ +
Sbjct  77   ASAITRLLDRVEKRGLLQRVRSSEDRRVVRLELTDEGRALTKRMPAIFRSVL---DEVLD  133

Query  124  KFTDEE  129
            FT EE
Sbjct  134  GFTPEE  139
```

>ref|YP_001961880.1| Transcriptional regulator, marR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)']
gb|ABZ93302.1| Transcriptional regulator, marR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)']
Length=145

GENE ID: 6388419 LBF_0770 | Transcriptional regulator, marR family [Leptospira biflexa serovar Patoc strain 'Patoc 1 (Ames)'] (10 or fewer PubMed links)

 Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 26/71 (36%), Positives = 45/71 (63%), Gaps = 1/71 (1%)

```
Query  31   SDVKLTSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDE  89
            +D+ LT  Q +++++ E+IST +KI +KL++     +T LK+L++ EL+   R  NDE
Sbjct  38   ADLGLTYPQYLVMLVMWEEKISTVSKIGDKLQLDSGTLTPLLKRLEQMELLDRMRNPNDE  97

Query  90   RVVLWSLTEKA  100
            R V   L++K
Sbjct  98   RSVNIVLSKKG  108
```

>ref|YP_001310724.1| MarR family transcriptional regulator [Clostridium beijerinckii NCIMB 8052]
gb|ABR35768.1| transcriptional regulator, MarR family [Clostridium beijerinckii NCIMB 8052]
Length=155

GENE ID: 5294814 Cbei_3649 | MarR family transcriptional regulator [Clostridium beijerinckii NCIMB 8052]

 Score = 47.4 bits (111), Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 30/109 (27%), Positives = 57/109 (52%), Gaps = 1/109 (0%)

```
Query  34   KLTSTQEHILMLLAEQISTN-AKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVV  92
            KLT +Q H + +    N  K++++L ++  A+TK KKL + +  + + + V
Sbjct  28   KLTFSQIHCIAAIEYIEDANITKLSQELGMTTGAITKMCKKLLNEGYVSKYQKEGNNKEV  87

Query  93   LWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALT  141
            + LTE + V + H  HEK+ + +++ ++ DEE+ I KFL +
Sbjct  88   YYDLTELGLNVCEIHNRIHEKSYNKKKDIIAQYNDEEKATILKFLHDMN  136
```

>ref|ZP_01065868.1| hypothetical transcriptional regulator, MarR family protein [Vibrio sp. MED222]
gb|EAQ52745.1| hypothetical transcriptional regulator, MarR family protein [Vibrio sp. MED222]
Length=301

 Score = 47.0 bits (110), Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 26/77 (33%), Positives = 45/77 (58%), Gaps = 0/77 (0%)

```
Query  25   LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSR  84
            +L K   D+ L   Q H L+ L +Q  T  ++A+KL I +  ++A+ L + LI++S
Sbjct  19   MLDKDCGDIALPPIQAHTLIELEQQPLTVNQLADKLNIDKSNASRAVNNLAKNSLIQTSP  78

Query  85   ATNDERVVLWSLTEKAV  101
            ND+R V+ S+TE+ +
Sbjct  79   HPNDKRSVVASVTEQGI  95
```

>ref|YP_140799.1| 🅖 MarR family transcriptional regulator [Streptococcus thermophilus CNRZ1066]

 gb|AAV61984.1| 🅖 transcriptional regulator, MarR family [Streptococcus thermophilus CNRZ1066]
Length=144

 GENE ID: 3167129 str0381 | MarR family transcriptional regulator
[Streptococcus thermophilus CNRZ1066] (10 or fewer PubMed links)

 Score = 47.0 bits (110), Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 30/90 (33%), Positives = 50/90 (55%), Gaps = 3/90 (3%)

```
Query  51  STNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH  110
               +T + +A +L ++   VT +L KL+++ I +R++ D RVV  SL++K   V + H
Sbjct  50  TTPSAVARELMLTLGTVTTSLNKLEKKGYIIRTRSSVDRRVVHLSLSKKGRLVYRLHRGF  109

Query  111  HEKTLSTYQELGNKFTDEEQEVISKFLSAL  140
            H+   S    +   F DEE +V+SK L  L
Sbjct  110  HK---SMVMRITEGFNDEELKVMSKGLENL  136
```


>ref|YP_143999.1| 🅖 MarR family transcriptional regulator [Thermus thermophilus HB8]

 dbj|BAD70556.1| 🅖 transcriptional regulator MarR family [Thermus thermophilus HB8]
Length=144

 GENE ID: 3168756 TTHA0733 | MarR family transcriptional regulator
[Thermus thermophilus HB8]

 Score = 46.6 bits (109), Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 34/109 (31%), Positives = 55/109 (50%), Gaps = 5/109 (4%)

```
Query  35  LTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLW  94
           L+ + H+L LLA+ +   +++AE L++ P+ V+  L  L+E+ L+K S     D R V
Sbjct  36  LSPRKAHLLGLLAKGVDLPSQLAELLEVHPSQVSHLLAALEEEGLVKRSPDPQDRRKVKL  95

Query  95  SLTEKAVPVAKEHATHHEKT-LSTYQELGNKFTDEEQEVISKFLSALTE  142
            LT    P  +E A  E   L+ +     + + EEQ   + L   LTE
Sbjct  96  FLT----PKGREAAARTEALWLAVFGRRLARLSPEEQAAFLRILRKLTE  140
```


>ref|YP_293371.1| 🅖 regulatory protein, MarR [Ralstonia eutropha JMP134]

 gb|AAZ65514.1| 🅖 regulatory protein, MarR [Ralstonia eutropha JMP134]
Length=150

 GENE ID: 3607869 Reut_C6203 | regulatory protein, MarR
[Ralstonia eutropha JMP134]

 Score = 46.6 bits (109), Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 32/112 (28%), Positives = 58/112 (51%), Gaps = 1/112 (0%)

```
Query  6   QIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNA-KIAEKLKISP  64
           +I Q +G +  A N  + +      D+ +T Q  IL+ L + ++T  ++++ L I
Sbjct  15  RITQSVGFFLNRARNTLLMEMDAALKDLDITGQQMGILLSLTQGVATTPFELSKVLGIDT  74

Query  65  AAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLS  116
            +T+ L KL+ + L+  SR+ +D RVV +LT+K   VA+    K L+
Sbjct  75  GLMTRMLDKLETKGLLSRSRSLDDRRVVNLTLTQKGQEVAERAPVVAPKVLN  126
```


>ref|YP_001307422.1| 🅖 MarR family transcriptional regulator [Clostridium beijerinckii NCIMB 8052]

 gb|ABR32466.1| 🅖 transcriptional regulator, MarR family [Clostridium beijerinckii NCIMB 8052]
Length=153

 GENE ID: 5291510 Cbei_0278 | MarR family transcriptional regulator
[Clostridium beijerinckii NCIMB 8052]

 Score = 46.6 bits (109), Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 30/114 (26%), Positives = 62/114 (54%), Gaps = 1/114 (0%)

```
Query  32   DVKLTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRATNDER  90
            D+ L ++ H++ + ++K   NA I+++L ++ A++K  KL ++ELIK +   + N++
Sbjct  40   DMGLMLSEIHVIDCIGKNQLINATFISKELNMTKGAISKITSKLLKKELIKGNHLENNKK  99

Query  91   VVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
            + ++LT + V K H+      + ++ +K+ EE +I+ FL  L  E
Sbjct  100  EIYYTLTAQGKEVFKVHEILHKIESEKFVKILSKYDKEELSIINSFLEDLISEL  153
```


>ref|ZP_02950515.1| transcriptional regulator, MarR family [Clostridium butyricum 5521]
 gb|EDT74473.1| transcriptional regulator, MarR family [Clostridium butyricum 5521]
Length=145

 Score = 46.2 bits (108), Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 32/86 (37%), Positives = 48/86 (55%), Gaps = 2/86 (2%)

```
Query  17  FAENKHEILLGK-CESDVKLTSTQE-HILMLLAEQISTNAKIAEKLKISPAAVTKALKKL  74
           +A ++  I L K C     LT TQ  +L+L ++ ST +I ++L +      +T LKK+
Sbjct  19  YAASREVIKLYKPCLDKFNLTYTQYVAMLVLWEDEKSTVKEIGKRLHLDSGTLTPLLKKM  78
```

```
Query  75   QEQELIKSSRATNDERVVLWSLTEKA  100
            +  ELIK  R  ND+RVV+  L EK
Sbjct  79   ESMELIKRYRDINDDRVVIVELAEKG  104
```

>ref|NP_266269.1| G transcription regulator [Lactococcus lactis subsp. lactis I11403]

 gb|AAK04211.1|AE006249_8 G transcriptional regulator [Lactococcus lactis subsp. lactis I11403]
Length=163

GENE ID: 1113719 rmaD | transcription regulator
[Lactococcus lactis subsp. lactis I11403] (10 or fewer PubMed links)

 Score = 46.2 bits (108), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query  41   HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA  100
            HIL  L ++  T  ++A KL ++     VT+A++ L + + + + ++ +D++ + + LT K
Sbjct  53   HILSALTKEDLTGIELATKLSVTRGGVTRAVQNLIKYQFLTTYQSESDKKKIFYHLTVKG  112

Query  101  VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS  138
            VA  H   H+      ++ +K+ ++E+ +I  FLS
Sbjct  113  RKVATIHDKMHKIMDIRLGQIFDKYNEQEKSIILSFLS  150
```

>ref|YP_002352539.1| G transcriptional regulator, MarR family [Dictyoglomus turgidum DSM 6724]

 gb|ACK41925.1| G transcriptional regulator, MarR family [Dictyoglomus turgidum DSM 6724]
Length=145

 GENE ID: 7081680 Dtur_0640 | transcriptional regulator, MarR family
[Dictyoglomus turgidum DSM 6724]

 Score = 46.2 bits (108), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 33/118 (27%), Positives = 63/118 (53%), Gaps = 8/118 (6%)

```
Query  31   SDVKLTSTQEHILMLLAEQIS-TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDE  89
            S +KL  Q  IL+LL+E+    T  +I E +KI P+ V  +++++++ L+ + R    D+
Sbjct  26   SGLKLYRGQAPILLLLSERDGLTQKEIVENMKIKPSTVAIMIRRMKKRGLVITKRDEKDK  85

Query  90   RVVLWSLTEKAVPVAKEHATHHEKTLSTYQE--LGNKFTDEEQEVISKFLSALTEEFQ  145
            R     LT++    ++       +KT   +E   GN FT+EE+E + +L + + +
Sbjct  86   RFSKVYLTDE----GRKFICKLKKTYKQLEEECFGN-FTEEERETLKNYLERIRDNLR  138
```

>ref|ZP_01854255.1| probable marR-family transcription regulator [Planctomyces maris DSM 8797]
 gb|EDL59963.1| probable marR-family transcription regulator [Planctomyces maris DSM 8797]
Length=159

 Score = 46.2 bits (108), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 29/83 (34%), Positives = 46/83 (55%), Gaps = 2/83 (2%)

```
Query  26   LGKCESDVKLTSTQEHILMLLA--EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSS  83
            G+  +  LT +Q ++L +L     +     + +IA ++    A+T  L +LQ QELIK +
Sbjct  38   FGRLFREYGLTPSQYNVLRILRGERKPMPSLEIANRMIQVVPAITGLLDRLQAQELIKRN  97

Query  84   RATNDERVVLWSLTEKAVPVAKE  106
            R T D RVV   +T KA+ + KE
Sbjct  98   RCTEDRRVVYIEITAKALKLLKE  120
```

>ref|YP_773280.1| G MarR family transcriptional regulator [Burkholderia ambifaria AMMD]

 gb|ABI86946.1| G transcriptional regulator, MarR family [Burkholderia ambifaria AMMD]
Length=164

 GENE ID: 4309612 Bamb_1388 | MarR family transcriptional regulator
[Burkholderia ambifaria AMMD]

 Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

```
Query  28   KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRAT  86
            + + ++ T TQ  +L ++A  + ST A++A + +AVT+ L +++++ L+    R+
Sbjct  40   RTQEELGITGTQASMLFMIAVGRCSTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI  99

Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF  144
            D RVV   LT++  +A+        L   EL  FT EE  +  L  +    +
Sbjct  100  EDRRVVRLELTDEGRALAERLPPVFRSVL---DELLGGFTPEEVGFLKSMLRRILSNY  154
```

>ref|ZP_01131766.1| transcriptional regulator, MarR family protein [Pseudoalteromonas tunicata D2]
 gb|EAR30132.1| transcriptional regulator, MarR family protein [Pseudoalteromonas tunicata D2]
Length=163

 Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 29/83 (34%), Positives = 47/83 (56%), Gaps = 1/83 (1%)

```
Query  28   KCESDVKLTSTQEHILMLLAEQISTNAK-IAEKLKISPAAVTKALKKLQEQELIKSSRAT  86
```

```
                K   +  LTS Q  +L  +++Q   , K IAE++  +S A +T  L +L+ +EL+   R+T
Sbjct  24   KLSKETGLTSPQLLVLQAISQQDGVMVKEIAEQINLSSATITSILDRLEIRELVIRERST   83

Query  87   NDERVVLWSLTEKAVPVAKEHAT  109
            D+R V  SLT+K    + K+  T
Sbjct  84   TDKRRVGISLTDKGFDIIKDSPT  106
```

>ref|ZP_00238819.1| transcriptional regulator, MarR family [Bacillus cereus G9241]
 gb|EAL13614.1| transcriptional regulator, MarR family [Bacillus cereus G9241]
Length=152

 Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 27/85 (31%), Positives = 49/85 (57%), Gaps = 1/85 (1%)

```
Query  35   LTSTQEHILMLLAEQISTNA-KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL   93
            LT Q +IL +L     ++ A K+A+K+ +  P+A+T  + +L +QEL++      +D RVV+
Sbjct  35   LTPPQFYILKILDHYGASRATKLAKKMYVKPSAITVMIDRLIDQELVERYHDKDDRRVVI   94

Query  94   WSLTEKAVPVAKEHATHHEKTLSTY  118
            LT+K      +E  T   + ++ Y
Sbjct  95   IELTKKGKARVEEAMTARNEHIAKY  119
```

>ref|YP_002467440.1| [G] transcriptional regulator, MarR family [Candidatus Methanosphaerula
palustris E1-9c]
 gb|ACL17717.1| [G] transcriptional regulator, MarR family [Candidatus Methanosphaerula
palustris E1-9c]
Length=159

 GENE ID: 7271351 Mpal_2438 | transcriptional regulator, MarR family
[Candidatus Methanosphaerula palustris E1-9c]

 Score = 45.8 bits (107), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 25/85 (29%), Positives = 47/85 (55%), Gaps = 0/85 (0%)

```
Query  56   IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTL   115
            IA+ L ++P+A ++A+ KL  + L+K R  +ER V   LT++     + H    H++
Sbjct  53   IADLLGVTPSAASQAVTKLAGRGLVKKVRGRKNEREVSLELTDQGWVAYRYHEQTHKEIY   112

Query  116  STYQELGNKFTDEEQEVISKFLSAL  140
            +   E     ++EE E+I++F +A
Sbjct  113  TRTTERVGPLSEEELELIARFFNAF   137
```

>ref|ZP_03547491.1| hypothetical protein BLAHAN_01259 [Blautia hansenii DSM 20583]
 gb|EED60137.1| hypothetical protein BLAHAN_01259 [Blautia hansenii DSM 20583]
Length=168

 Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 32/105 (30%), Positives = 53/105 (50%), Gaps = 4/105 (3%)

```
Query  41   HILMLLAEQISTN-AKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEK   99
            HI+  + E+ + N + +A+ L ++    +T A+ L ++   R+  D RVVL SLT K
Sbjct  60   HIMEAIGEENAKNMSSVAKLLSVTVGTLTIAINGLVKKGYVARERSEEDRRVVLISLTGK   119

Query  100  AVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF   144
               + H  H+  +   Q L    DE+QE++ K L   L E F
Sbjct  120  GRKANEHHKKFHDGMI---QALLKDLDDEQQEILVKSLLNLREFF   161
```

>ref|ZP_02891041.1| transcriptional regulator, MarR family [Burkholderia ambifaria
IOP40-10]
 gb|EDT03378.1| transcriptional regulator, MarR family [Burkholderia ambifaria
IOP40-10]
Length=163

 Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

```
Query  28   KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRAT   86
            + + ++ +T TQ  +L ++A  + ST A++A  L+ + +AVT+ L +++++ L+   R+
Sbjct  40   RTQEELGITGTQASMLFMIAVGKCSTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI   99

Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF   144
            + D RVV  LT++    +A+     L    EL   FT EE   +  L +   +
Sbjct  100  EDRRVVRLELTDEGRELAERLPPVFRSVL---DELLGGFTPEEVGFLKSMLRRILSNY   154
```

>ref|YP_001808132.1| [G] MarR family transcriptional regulator [Burkholderia ambifaria
MC40-6]
 gb|ACB63916.1| [G] transcriptional regulator, MarR family [Burkholderia ambifaria
MC40-6]
Length=164

 GENE ID: 6177160 BamMC406_1428 | MarR family transcriptional regulator
[Burkholderia ambifaria MC40-6]

 Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

```
Query  28   KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRAT   86
            + + ++ +T TQ  +L ++A  + ST A++A  + I  +AVT+ L +++++ L+   R+
Sbjct  40   RTQEELGITGTQASMLFMIAVGKCSTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI   99
```

```
Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF   144
            D RVV   LT++   +A+        L   EL   FT EE   +   L  +   +
Sbjct  100  EDRRVVRLELTDEGRALAERLPPVFRSVL---DELLGGFTPEEVGFLKSMLRRILSNY   154
```

>ref|ZP_02906301.1| transcriptional regulator, MarR family [Burkholderia ambifaria
MEX-5]
  gb|EDT42559.1| transcriptional regulator, MarR family [Burkholderia ambifaria
MEX-5]
Length=164

  Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
  Identities = 31/118 (26%), Positives = 59/118 (50%), Gaps = 4/118 (3%)

```
Query  28   KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRAT   86
            + + ++ +T TQ +L ++A  + ST A++A +  I  +AVT+ L +++++ L+   R+
Sbjct  40   RTQEELGITGTQASMLFMIAVGKCSTAAELAREYGIDASAVTRLLDRVEKRGLLSRVRSI   99
```

```
Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF   144
            D RVV   LT++   +A+        L   EL   FT EE   +   L  +   +
Sbjct  100  EDRRVVRLELTDEGRALAERLPPVFRSVL---DELLGGFTPEEVGFLKSMLRRILSNY   154
```

>ref|ZP_02362996.1| transcriptional regulator, MarR family protein [Burkholderia
oklahomensis C6786]
Length=165

  Score = 45.4 bits (106), Expect = 0.001, Method: Compositional matrix adjust.
  Identities = 31/126 (24%), Positives = 69/126 (54%), Gaps = 5/126 (3%)

```
Query  6    QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS   63
            QI+  +G +M   ++      ++   + ++++ +T TQ +L +LA  + ST A++A +  I
Sbjct  17   QINDSVGYLMSRVKSLMTNMVTQRTQTELGITGTQATMLFMLAVGKCSTAAELAREYGID   76
```

```
Query  64   PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN   123
            +A+T+ L +++++ L++   R++ D RVV   LT++   + +        L      ++ +
Sbjct  77   ASAITRLLDRVEKRGLLQRVRSSEDRRVVRLELTDEGRDLTRRMPAIFRSVL---DQVLD   133
```

```
Query  124  KFTDEE   129
            FT EE
Sbjct  134  GFTPEE   139
```

>ref|NP_977055.1| [G] MarR family transcriptional regulator [Bacillus cereus ATCC 10987]
  gb|AAS39663.1| [G] transcriptional regulator, MarR family [Bacillus cereus ATCC
10987]
Length=152

  GENE ID: 2747926 BCE_0730 | MarR family transcriptional regulator
[Bacillus cereus ATCC 10987] (10 or fewer PubMed links)

  Score = 45.4 bits (106), Expect = 0.002, Method: Compositional matrix adjust.
  Identities = 27/85 (31%), Positives = 49/85 (57%), Gaps = 1/85 (1%)

```
Query  35   LTSTQEHILMLLAEQISTNA-KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVL   93
            LT  Q +IL +L    ++ A K+A+K+ + P+A+T  + +L +QEL++     +D RVV+
Sbjct  35   LTPPQFYILKILDHYGASRATKLAKKMYVKPSAITVMIDRLIDQELVERYHDKDDRRVVV   94
```

```
Query  94   WSLTEKAVPVAKEHATHHEKTLSTY   118
            +++K    +E  T  + ++ Y
Sbjct  95   IELTKKGKARVEEAMTARNEHIAKY   119
```

>ref|NP_782475.1| [G] MarR family transcriptional regulator [Clostridium tetani E88]
  gb|AAO36412.1| [G] transcriptional regulator, marR family [Clostridium tetani E88]
Length=154

  GENE ID: 1058804 marR | MarR family transcriptional regulator
[Clostridium tetani E88] (10 or fewer PubMed links)

  Score = 45.4 bits (106), Expect = 0.002, Method: Compositional matrix adjust.
  Identities = 25/91 (27%), Positives = 50/91 (54%), Gaps = 0/91 (0%)

```
Query  51   STNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATH   110
            +   +IA  L I+ +AV+K +++LQ++ LI SS+     ++++LT +     + K+H
Sbjct  50   ANGTQIANYLNITRSAVSKIIRRLQKENLIISSQKPDNKKEIFYTLTNEGNNIFKQHKQA   109
```

```
Query  111  HEKTLSTYQELGNKFTDEEQEVISKFLSALT   141
            HEK      +   E+E + KFL
Sbjct  110  HEKWEIRDTKFLKTISTNEKETVFKFLKKFN   140
```

>ref|ZP_03570809.1| transcriptional regulator, MarR family [Burkholderia multivorans
CGD2M]
  ref|ZP_03577696.1| transcriptional regulator, MarR family [Burkholderia multivorans
CGD2]
  ref|ZP_03586132.1| transcriptional regulator, MarR family [Burkholderia multivorans
CGD1]
  gb|EED99839.1| transcriptional regulator, MarR family [Burkholderia multivorans
CGD1]
  gb|EEE07966.1| transcriptional regulator, MarR family [Burkholderia multivorans
CGD2]
  gb|EEE14096.1| transcriptional regulator, MarR family [Burkholderia multivorans
CGD2M]
Length=164

```
 Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 32/118 (27%), Positives = 60/118 (50%), Gaps = 4/118 (3%)

Query  28   KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRAT   86
            + + ++ +T TQ  +L ++A  + ST A++A +   I  +AVT+ L +++++ L+   R+
Sbjct  40   RTQEELGITGTQASMLFMIAVGKCSTAAELAREYAIDASAVTRLLDRVEKRGLLCRVRSV   99

Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF    144
            D RVV   LT++   +A+         L  Q LG  FT EE   + L  +   +
Sbjct  100  EDRRVVRLELTDEGRALAERLPAIFRSVLD--QLLGG-FTPEEVGFLKSMLRRILSNY    154
```

>ref|YP_001119315.1| 🅖 MarR family transcriptional regulator [Burkholderia vietnamiensis G4]

  gb|ABO54480.1| 🅖 transcriptional regulator, MarR family [Burkholderia vietnamiensis G4]
Length=163

  GENE ID: 4953186 Bcep1808_1472 | MarR family transcriptional regulator [Burkholderia vietnamiensis G4]

```
 Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 35/126 (27%), Positives = 66/126 (52%), Gaps = 5/126 (3%)

Query  6    QIDQFLGTIMQFAENKHEILLG-KCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS   63
            QI+  +G +M   ++   L+ + + ++ +T TQ  +L ++A  + ST A++A + I
Sbjct  17   QINDSVGYLMSRVKSVMTNLVTQRTQEELGITGTQASMLFMIAVGKCSTAAELAREYGID   76

Query  64   PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN   123
            +AVT+ L +++++ L+   R+   D RVV   LT++   +A+         L  EL
Sbjct  77   ASAVTRLLDRVEKRGLLSRVRSIEDRRVVRLELTDEGRALAERLPPVFRSVL---DELLE   133

Query  124  KFTDEE   129
            FT EE
Sbjct  134  GFTPEE   139
```

>ref|YP_002418276.1| 🅖 Histone acetyltransferase HPA2 and related acetyltransferases [Vibrio splendidus LGP32]

  emb|CAV19992.1| 🅖 Histone acetyltransferase HPA2 and related acetyltransferases [Vibrio splendidus LGP32]
Length=301

  GENE ID: 7162224 VS_2735 | Histone acetyltransferase HPA2 and related acetyltransferases [Vibrio splendidus LGP32]

```
 Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 35/117 (29%), Positives = 60/117 (51%), Gaps = 1/117 (0%)

Query  25   LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSR   84
            +L K · D+ L  Q H L+ L +Q  T  ++A+KL I  + ++A+ L + LI++S
Sbjct  19   MLDKDCGDIALPPIQAHTLIELEQQPLTVNQLADKLNIDKSNASRAVNNLAKNSLIQTSP   78

Query  85   ATNDERVVLWSLTEKA-VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSAL    140
            ND+R V+ S+T++    +AK H  ++    S + L    T +    I +L AL
Sbjct  79   HPNDKRSVVASVTDQGKNTLAKLHNQQNQFYDSVLEHLTEAETQQVSGGIEHYLKAL    135
```

>ref|ZP_02355848.1| transcriptional regulator, MarR family protein [Burkholderia oklahomensis EO147]
Length=165

```
 Score = 45.1 bits (105), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 31/126 (24%), Positives = 69/126 (54%), Gaps = 5/126 (3%)

Query  6    QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS   63
            QI+  +G +M   ++    ++   + + +T TQ  +L ++A  + ST A++A + I
Sbjct  17   QINDSVGYLMSRVKSLMTNMVTQRTQTELGITGTQATMLFMLAVGKCSTAAELAREYGID   76

Query  64   PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN   123
            +A+T+ L +++++ L++   R++  D RVV   LT++  + +         L   ++ +
Sbjct  77   ASAITRLLDRVEKRGLLQRVRSSEDRRVVRLELTDEGRELTRRMPAIFRSVL---DQVLD   133

Query  124  KFTDEE   129
            FT EE
Sbjct  134  GFTPEE   139
```

>ref|YP_443075.1| 🅖 MarR family transcriptional regulator [Burkholderia thailandensis E264]
  ref|ZP_02374954.1| transcriptional regulator, MarR family protein [Burkholderia thailandensis TXDOH]
  ref|ZP_02388872.1| transcriptional regulator, MarR family protein [Burkholderia thailandensis Bt4]
  gb|ABC39239.1| 🅖 transcriptional regulator, MarR family [Burkholderia thailandensis E264]
Length=165

  GENE ID: 3849294 BTH_I2558 | MarR family transcriptional regulator [Burkholderia thailandensis E264] (10 or fewer PubMed links)

```
 Score = 44.7 bits (104), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 33/126 (26%), Positives = 67/126 (53%), Gaps = 5/126 (3%)
```

```
Query  6    QIDQFLGTIMQFAEN-KHEILLGKCESDVKLTSTQEHILMLLA-EQISTNAKIAEKLKIS  63
            QI+  +G +M  ++      ++  + ++++ +T TQ  +L +LA  + ST A++A + I
Sbjct  17   QINDSVGYLMSRVKSLMTNMVTQRTQTELGITGTQATMLFMLAVGKCSTAAELAREYGID  76

Query  64   PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN  123
            +A+T+ L +++++ L++  R++ D RVV   LT++  + K       L    E
Sbjct  77   ASAITRLLDRVEKRGLLQRVRSSEDRRVVRLELTDEGRELTKRMPEIFRSVLDQVLE---  133

Query  124  KFTDEE  129
            FT EE
Sbjct  134  GFTPEE  139
```

>**ref|ZP_02633998.1|** transcriptional regulator, MarR family [Clostridium perfringens
E str. JGS1987]
  ref|ZP_02636384.1| transcriptional regulator, MarR family [Clostridium perfringens
B str. ATCC 3626]
  ref|ZP_02643088.1| transcriptional regulator, MarR family [Clostridium perfringens
NCTC 8239]
  7 more sequence titles

ref|ZP_02629009.2| transcriptional regulator, MarR family [Clostridium perfringens
C str. JGS1495]
  ref|ZP_02954000.1| transcriptional regulator, MarR family [Clostridium perfringens
D str. JGS1721]
  gb|EDS81585.1| transcriptional regulator, MarR family [Clostridium perfringens
C str. JGS1495]
  gb|EDT13394.1| transcriptional regulator, MarR family [Clostridium perfringens
E str. JGS1987]
  gb|EDT23419.1| transcriptional regulator, MarR family [Clostridium perfringens
B str. ATCC 3626]
  gb|EDT71039.1| transcriptional regulator, MarR family [Clostridium perfringens
D str. JGS1721]
  gb|EDT77904.1| transcriptional regulator, MarR family [Clostridium perfringens
NCTC 8239]
Length=154

 Score = 44.7 bits (104), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 33/99 (33%), Positives = 50/99 (50%), Gaps = 5/99 (5%)

```
Query  48   EQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEH  107
            E+  T +++A  LKI+   +T A+ KL ++  +   R   D RVV+  LTEK    K H
Sbjct  49   EKARTMSEVALDLKITVGTLTTAINKLIKKGYVNRRRIEEDRRVVMIELTEKGTLAYKVH  108

Query  108  ATHHEKTLS-TYQELGNKFTDEEQEVISKFLSALTEEFQ  145
             HE+ +    +ELG    E+EV+  L  L + FQ
Sbjct  109  EKFHEEMIDHVLEELGVS----EEEVLISSLDKLDKFFQ  143
```

>**ref|YP_001374721.1|** 🄶 MarR family transcriptional regulator [Bacillus cereus subsp.
cytotoxis NVH 391-98]
  gb|ABS21726.1| 🄶 transcriptional regulator, MarR family [Bacillus cereus subsp.
cytotoxis NVH 391-98]
Length=136

 GENE ID: 5344927 Bcer98_1405 | MarR family transcriptional regulator
[Bacillus cereus subsp. cytotoxis NVH 391-98]

 Score = 44.7 bits (104), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 37/119 (31%), Positives = 62/119 (52%), Gaps = 4/119 (3%)

```
Query  28   KCESDVKLTSTQEHILMLLAEQISTN-AKIAEKLKISPAAVTKALKKLQEQELIKSSRAT  86
            +CE +  L+    IL + + +  T  +KIA +L +S    ++ +K+L +++LI    R
Sbjct  16   RCEYENNLSHQAIRILQITSREAETTISKIASELNLSHNTASEHVKRLIQKDLILKERNK  75

Query  87   NDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEFQ  145
            DERVV  +LT K      +H   EK L    L ++ + EEQ++I +  S L +E Q
Sbjct  76   KDERVVNLALTAKGKEALIKHTLLDEKKLKI---LESQLSKEEQQIIEQAFSILAKEAQ  131
```

>**ref|YP_819461.1|** 🄶 transcriptional regulator [Leuconostoc mesenteroides subsp. mesenteroides
ATCC 8293]
  gb|ABJ63088.1| 🄶 Transcriptional regulator [Leuconostoc mesenteroides subsp. mesenteroides
ATCC 8293]
Length=146

 GENE ID: 4423731 LEUM_2018 | transcriptional regulator
[Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]
(10 or fewer PubMed links)

 Score = 44.7 bits (104), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 30/84 (35%), Positives = 46/84 (54%), Gaps = 5/84 (5%)

```
Query  34   KLTSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVV  92
            K+ STQ H+LMLL   Q  TN ++A + +S A+TKA+K L   + +    +D+R
Sbjct  32   KINSTQAHLLMLLKILQSQTNTELAAAMNLSKPAITKAIKNLMRYHYVIAVVDDSDKRST  91

Query  93   LWSLTEKAVPVA----KEHATHHE  112
             + LTE    +A    + HAT H+
Sbjct  92   HYLLTEDGEKLAQLHEQAHATMHD  115
```

>**ref|ZP_02027443.1|** hypothetical protein EUBVEN_02713 [Eubacterium ventriosum ATCC
27560]

gb|EDM50067.1| hypothetical protein ·EUBVEN_02713 [Eubacterium ventriosum ATCC 27560]
Length=151

Score = 44.7 bits (104),   Expect = 0.003, Method: Compositional matrix adjust.
Identities = 27/90 (30%), Positives = 53/90 (58%), Gaps = 3/90 (3%)

```
Query  56   IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTL  115
            IA+K+KI+  ++T ++  L ++   ++ +R+  D R+V  +LTEK +   K H   HEK
Sbjct  60   IAKKMKITVGSLTTSMNSLVKKHYVERNRSEEDRRIVNITLTEKGIKAYKHHEEFHEK--  117

Query  116  STYQELGNKFTDEEQEVISKFLSALTEEFQ  145
                Q   ++ +++E +V+ K L+ L++ F
Sbjct  118  -MSQAAISEMSEDEVKVLLKSLNNLSKFFH  146
```

Select All Get selected sequences Distance tree of results

CABINET

O R E S

36, rue de St Pétersbourg
75008 PARIS
Tél. (33) 01 53 21 11 00
Fax (33) 01 53 21 08 88
(33) 01 53 21 08 63
http://www.cabinet-ores.com
E-mail : ores@cabinet-ores.com

By facsimile
+ confirmation by e-mail

THE NATH LAW GROUP
112 South West Street
US-ALEXANDRIA, VA 22314
ETATS-UNIS D'AMERIQUE

Attention : M. William E. BEAUMONT

BÉATRICE ORÈS ①③
PHARMACIEN DIPLÔMÉ
DE LA FACULTÉ DE PARIS

IRÈNE ORÈS ❀ ①②④
LICENCIÉE ES-SCIENCES
LICENCIÉE EN DROIT
ANCIEN CONSEIL JURIDIQUE

BERNARD ORÈS ①②④
INGÉNIEUR CHIMISTE ESCIL
LICENCIÉ ES-SCIENCES

MARIE-JOSÉ VIALLE-PRESLES ①②④
DOCTEUR EN BIOCHIMIE

PHILIPPE JACQUARD ①②
INGÉNIEUR INPG

HÉLÈNE LEBLOIS-PRÉHAUD ②④
DOCTEUR EN MICROBIOLOGIE
DOCTEUR VÉTÉRINAIRE

VALÉRIE CORIZZI ①②
INGÉNIEUR ÉCOLE POLYTECHNIQUE (PARIS)
DOCTEUR EN CHIMIE

XAVIER RATABOUL ②④
INGÉNIEUR ENSAT

ENRICO PRIORI ②④
INGÉNIEUR ECOLE CENTRALE PARIS
DOCTEUR EN PHYSIQUE

MICHEL BOLINCHES ①②
INGÉNIEUR ENSIACET

VÉRONIQUE MARCADÉ ①②
INGÉNIEUR ÉCOLE CENTRALE PARIS
DOCTEUR EN BIOLOGIE

CHANTAL NOËL ①②
INGÉNIEUR ESCOM

HÉLÈNE CORRET ①②③
INGÉNIEUR ÉCOLE CENTRALE LYON
DESS DE DROIT DE LA PROP. INDUSTRIELLE

XAVIER RANÇON ②④
INGÉNIEUR AGRONOME INA P-G
MAÎTRE ES-SCIENCES

DEAN THOMAS ①②⑤
DOCTEUR EN GÉNÉTIQUE MOLÉCULAIRE
& BIOLOGIE MATHÉMATIQUE

CLAIRE BERNSTEIN ②④
INGÉNIEUR ENSAIA

SANDRA MENA ②④
INGÉNIEUR ESCOM

DAVID GHIBAUDO ④
DOCTEUR EN MICROBIOLOGIE/VIROLOGIE

SERVICE JURIDIQUE

NATHALIE ROUSSET ①③
MAÎTRE EN DROIT DES AFFAIRES

GENEVIÈVE VU THANH ①③
LICENCIÉE EN DROIT DES AFFAIRES

FABRICE PIGEAUX ①③
DESS DROIT DU MSI

ELISABETH FOSSOT ①③
I.E.P. STRASBOURG - MAÎTRE EN DROIT
DESS « ACCORDS ET PROPRIÉTÉ INDUSTRIELLE »

SERVICE ADMINISTRATIF

ERIC ANDRIEU
DIRECTEUR ADMINISTRATIF ET FINANCIER

ANNIE LECUYER
RESPONSABLE ADMINISTRATIVE M

DOCUMENTATION
& INFORMATIQUE

FABRICE SAUSSEREAU
DEUST DROIT INFORMATIQUE
ET SYSTEME D'INFORMATION

① CONSEIL EN PROPRIÉTÉ INDUSTRIELLE
② MANDATAIRE EN BREVETS EUROPÉENS
③ MANDATAIRE AGRÉÉ PRÈS L'OHMI
④ DIPLÔMÉ(E) DU CEIPI
⑤ IRISH & BRITISH PATENT ATTORNEY

S.A. au Capital de 360 000,00 €
380 823 179 R.C.S. Paris

Paris, March 5, 2009

UNITED STATES OF AMERICA - PATENT APPLICATION No. 10/525,449
filed on : August 29, 2003
In the name of: INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE.
For :   « Zinc-regulated prokaryotic expression cassettes. »
Invention : POQUET Isabelle, LLULL Daniel

Y/Ref.: 1169-034   O/Ref.: MJP/DG/md - F053900116/US/PCT

Dear Sir,

We refer to your letter of October 31, 2008 transmitting us the 1st Office Action issued in relation with the above-referred application.

We have discussed this case with the applicant, and beg you to find herein enclosed our comments and instructions concerning this application.

Since we believe that an interview with the Examiner will be necessary in order to discuss the objections and the possible amendments to the claims, you may request a third month extension of time.

Please **acknowledge receipt** of this letter by return.

In the meantime, we are,

Very truly yours,

M.J. VIALLE-PRESLES   **B. ORES**

Encl. :   - Memorandum, and
- Annexes (only by e-mail).

U.S Application 10/1525449

MEMORANDUM OF INSTRUCTIONS FOR RESPONDING THE OFFICE ACTION OF OCTOBER 7, 2008

1) Claims objections:
We beg you to amend the claims as requested by the Examiner. Concerning claim 15, it differs from claim 12 in that the expression cassette does not comprise the sequence encoding the ZitR repressor (cf § [0025] to [0027] of the instant application), and can be used to obtain constitutive expression of a protein of interest in bacterial strains wherein the endogenous ZitR repressor is inactivated (cf. § [0053] of the instant application)

2) Rejection under 35 USC § 112.
We wish to point out that the definition "at least 80% identity with the *Lactococcus lactis* ZitR protein GENBANK AAK06214" does not encompass a broad variety of proteins.
The results of BLAST searchs using GENBANK AAK06214 as a query are enclosed therein. A first search was performed against all the protein sequences available in the nr database (all known protein sequences, including the complete sequences of various bacteria). The enclosed results (Annex 1) show that the only proteins having more than 80% identity with GENBANK AAK06214 (which is the ZitR protein of *Lactococcus lactis* subsp. *lactis* Il1403), are the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* SK11 (89% identity) and the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* MG1363 (88% identity).
A second search was performed against the whole genome sequences of *Lactococcus lactis* subsp. *lactis* Il1403, *Lactococcus lactis* subsp. *cremoris* SK11 and *Lactococcus lactis* subsp. *cremoris* MG1363. The enclosed results (Annex 2) show that the only lactococcal proteins having more than 80% identity with GENBANK AAK06214, are the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* SK11 (89% identity) and the ZitR proteins of *Lactococcus lactis* subsp. *cremoris* MG1363 (88% identity).
Therefore, obtaining a nucleotide sequence encoding a protein having more than 80% identity with GENBANK AAK06214 would not have required require undue experimentation for one of skill in the art. He would have easily obtained it by routine screening of a lactococcal DNA library with a probe derived from the nucleotide sequence encoding GENBANK AAK06214 (or from nucleotides 357-794 of SEQ ID NO:2), and would inevitably have found the orthologs of GENBANK AAK06214.
We beg you to request an interview with the Examiner in order to discuss this issue of enablement. If necessary, you may amend paragraph b) of claim 12 so as to

specify that the polypeptide is a lactococcal polypeptide, and/or to indicate a higher percent of identity (85% rather than 80%) with GENBANK AAK06214.

3) Rejection under 35 USC § 102.
We beg you to insert in claims 12 and 15 the same disclaimer as in claim 18, which excludes the cassette and vector of POQUET et al.

BLAST Basic Local Alignment Search Tool

•

gb|AAK06214| (145 letters)

Results for: gb|AAK06214.1 zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis Il1403](145aa)
Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show
BLAST results for.

Query ID
 gi|12725171|gb|AAK06214.1|AE006439_11
Description
 zinc transport transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Molecule type
 amino acid
Query Length
 145

Database Name
 3 databases
Description
Program
 BLASTP 2.2.19+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.
Reference - compositional score matrix adjustment
Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A.
Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices",
FEBS J. 272:5101-5109.
Other reports: Search Summary [Taxonomy reports] [Distance tree of results]

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Low Complexity Filter	Yes
Filter string	L;
Genetic Code	1
Window Size	40

Database

Posted date	Mar 2, 2009 5:57 PM
Number of letters	2,055,736
Number of sequences	7,259
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.310848	0.267
K	0.124161	0.041

H   0.32399   0.14

Results Statistics

Length adjustment	78 .
Effective length of query	67
Effective length of database	1489534
Effective search space	99798778
Effective search space used	99798778

Graphic Summary

Distribution of 58 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Descriptions

Sequences producing significant alignments:	Score (Bits)	E Value	
ref|NP_268273.1| zinc transport transcription regulator [Lact...	291	2e-80	G
ref|YP_811979.1| transcriptional regulator [Lactococcus lacti...	268	2e-73	G
ref|YP_001033643.1| transcriptional regulator of the zit oper...	267	3e-73	G
ref|YP_001033131.1| MarR family transcriptional regulator [La...	53.9	6e-09	G
ref|YP_808725.1| transcriptional regulator [Lactococcus lacti...	51.2	4e-08	G
ref|NP_266864.1| transcription regulator [Lactococcus lactis ...	51.2	4e-08	G
ref|YP_808147.1| transcriptional regulator [Lactococcus lacti...	50.4	7e-08	G
ref|YP_001031482.1| MarR family transcriptional regulator [La...	49.3	1e-07	G
ref|NP_266269.1| transcription regulator [Lactococcus lactis ...	46.2	1e-06	G
ref|NP_267626.1| transcription regulator [Lactococcus lactis ...	41.2	4e-05	G
ref|YP_001032345.1| MarR family transcriptional regulator [La...	38.9	2e-04	G
ref|YP_806479.1| transcriptional regulator [Lactococcus lacti...	37.0	9e-04	G
ref|NP_266463.1| MarR family transcriptional regulator [Lacto...	36.2	0.001	G
ref|NP_266747.1| transcription regulator [Lactococcus lactis ...	35.8	0.002	G
ref|YP_001031675.1| MarR family transcriptional regulator [La...	35.4	0.002	G
ref|NP_266396.1| MarR family transcriptional regulator [Lacto...	35.4	0.002	G
ref|YP_808372.1| MarR family transcriptional regulator [Lacto...	35.4	0.002	G
ref|YP_001031774.1| transcriptional regulator [Lactococcus la...	35.0	0.003	G
ref|YP_001031373.1| putative transcriptional regulator [Lacto...	33.3	0.017	G
ref|YP_808573.1| BadM/Rrf2 family transcriptional regulator [...	33.3	0.018	G
ref|NP_266714.1| hypothetical protein L153086 [Lactococcus la...	33.3	0.018	G
ref|YP_001033090.1| MarR family transcriptional regulator [La...	31.6	0.031	G
ref|YP_808765.1| MarR family transcriptional regulator [Lacto...	31.6	0.034	G
ref|YP_808795.1| MarR family transcriptional regulator [Lacto...	31.2	0.044	G
ref|NP_266926.1| MarR family transcriptional regulator [Lacto...	31.2	0.045	G
ref|YP_001032909.1| MarR family transcriptional regulator [La...	28.9	0.18	G
ref|YP_001032520.1| MarR family transcriptional regulator [La...	28.1	0.31	G
ref|NP_267064.1| transcription regulator [Lactococcus lactis ...	28.1	0.35	G
ref|YP_001032593.1| transcriptional regulator [Lactococcus la...	28.1	0.38	G
ref|YP_809312.1| Mn-dependent transcriptional regulator [Lact...	28.1	0.38	G
ref|NP_267461.1| transcription regulator [Lactococcus lactis ...	27.7	0.42	G
ref|NP_267696.1| transcription regulator [Lactococcus lactis ...	27.3	0.61	G
ref|NP_266753.1| NADPH-flavin oxidoreductase [Lactococcus lac...	27.3	0.67	G
ref|NP_267412.1| metalloregulator [Lactococcus lactis subsp. ...	26.6	1.1	G
ref|YP_001031697.1| putative cobalt ABC transporter ATP-bindi...	26.2	1.2	G
ref|NP_266973.1| quinone oxidoreductase [Lactococcus lactis s...	25.4	2.4	G
ref|NP_268402.1| alkylphosphonate uptake protein [Lactococcus...	25.4	2.4	G
ref|YP_808109.1| transcriptional repressor CodY [Lactococcus ...	24.6	3.4	G
ref|YP_001031533.1| transcriptional repressor CodY [Lactococc...	24.6	3.4	G
ref|NP_266317.1| transcriptional repressor CodY [Lactococcus ...	24.6	3.5	G
ref|NP_266838.1| intercellular adhesion protein [Lactococcus ...	24.6	3.6	G
ref|NP_266710.1| transcription regulator [Lactococcus lactis ...	24.6	3.6	G
ref|NP_266438.1| amino acid amidohydrolase [Lactococcus lacti...	24.6	4.1	G
ref|YP_809446.1| lysyl-tRNA synthetase [Lactococcus lactis su...	24.6	4.3	G
ref|YP_001031741.1| lysyl-tRNA synthetase [Lactococcus lactis...	24.3	4.7	G
ref|NP_266529.1| lysyl-tRNA synthetase [Lactococcus lactis su...	24.3	4.7	G
ref|YP_001031907.1| NADPH-flavin oxidoreductase [Lactococcus ...	24.3	5.2	G
ref|YP_808603.1| NADPH-flavin oxidoreductase [Lactococcus lac...	24.3	5.5	G
ref|NP_268393.1| exported serine protease [Lactococcus lactis...	23.9	6.1	G
ref|YP_001033660.1| housekeeping protease [Lactococcus lactis...	23.9	6.5	G
ref|YP_811995.1| trypsin-like serine protease [Lactococcus la...	23.9	6.6	G
ref|NP_268332.1| hypothetical protein L35545 [Lactococcus lac...	23.5	7.5	G

ref|NP_268337.1| hypothetical protein L39650 [Lactococcus lac...	23.5	7.7	G
ref|YP_001032772.1| superfamily II DNA/RNA helicase [Lactococ...	23.5	7.8	G
ref|YP_001033122.1| quinone oxidoreductase [Lactococcus lacti...	23.5	9.3	G
ref|YP_808733.1| quinone oxidoreductase [Lactococcus lactis s...	23.5	9.3	G
ref|YP_796521.1| hypothetical protein LACR_C57 [Lactococcus l...	23.5	9.5	G
ref|YP_811995.1| hypothetical protein LACR_2554 [Lactococcus ...	23.1	10.0	G

Alignments Select All Get selected sequences Distance tree of results

>ref|NP_268273.1| G zinc transport transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=145

 GENE ID: 1115793 zitR | zinc transport transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 291 bits (744), Expect = 2e-80, Method: Compositional matrix adjust.
 Identities = 145/145 (100%), Positives = 145/145 (100%), Gaps = 0/145 (0%)

Query 1   MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
            MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL
Sbjct 1   MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60

Query 61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120
            KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE
Sbjct 61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120

Query 121 LGNKFTDEEQEVISKFLSALTEEFQ 145
            LGNKFTDEEQEVISKFLSALTEEFQ
Sbjct 121 LGNKFTDEEQEVISKFLSALTEEFQ 145

>ref|YP_811979.1| G transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=145

 GENE ID: 4433026 LACR_2420 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 268 bits (685), Expect = 2e-73, Method: Compositional matrix adjust.
 Identities = 130/145 (89%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

Query 1   MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
            MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA ++STNA+IAE+L
Sbjct 1   MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILAAEVSTNARIAEQL 60

Query 61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120
            KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHA HHEKTLSTYQE
Sbjct 61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHAAHHEKTLSTYQE 120

Query 121 LGNKFTDEEQEVISKFLSALTEEFQ 145
            LG+KFTDEEQ+VIS+FLS LTEEF+
Sbjct 121 LGDKFTDEEQKVISQFLSVLTEEFR 145

>ref|YP_001033643.1| G transcriptional regulator of the zit operon [Lactococcus lactis subsp. cremoris MG1363]
Length=145

 GENE ID: 4799067 zitR | transcriptional regulator of the zit operon
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 267 bits (682), Expect = 3e-73, Method: Compositional matrix adjust.
 Identities = 129/145 (88%), Positives = 141/145 (97%), Gaps = 0/145 (0%)

Query 1   MSLANQIDQFLGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKL 60
            MSLANQIDQFLG IMQFAENKHEILLG+CES+VKLTSTQEHILM+LA ++STNA+IAE+L
Sbjct 1   MSLANQIDQFLGAIMQFAENKHEILLGECESNVKLTSTQEHILMILAAEVSTNARIAEQL 60

Query 61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQE 120
            KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA+PVAKEHA HHEKTLSTYQE
Sbjct 61   KISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAIPVAKEHAAHHEKTLSTYQE 120

Query 121 LGNKFTDEEQEVISKFLSALTEEFQ 145
            LG+KFTDEEQ+VIS+FLS LTEEF+
Sbjct 121 LGDKFTDEEQKVISQFLSVLTEEFR 145

>ref|YP_001033131.1| G MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=295

GENE ID: 4797387 rmaB | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 53.9 bits (128), Expect = 6e-09, Method: Compositional matrix adjust.
 Identities = 38/101 (37%), Positives = 54/101 (53%), Gaps = 3/101 (2%)

```
Query   42   ILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAV   101
             ++ L  E    TNA+IAE L I P++VT  +K+L+E E++    +  ND+RV    LTEK
Sbjct   47   LVELWNEDGLTNAEIAELLDIKPSSVTTQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGR   106

Query   102  PVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTE   142
                 +   T H    T   GN  TDEEQE ++  +  L E
Sbjct   107  EAQETRDTMHNDISETI--FGN-LTDEEQEQLANLMEKLVE   144
```

>**ref|YP_808725.1|** [G] transcriptional regulator [Lactococcus lactis subsp. cremoris
SK11]
Length=292

GENE ID: 4432217 LACR_0742 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 51.2 bits (121), Expect = 4e-08, Method: Compositional matrix adjust.
 Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

```
Query   52   TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHH   111
             TNA+IAE L I P++VT  +K+L+E E++    +  ND+RV    LTEK    +   T H
Sbjct   57   TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVNRIFLTEKGREAQETRDTMH   116

Query   112  EKTLSTYQELGNKFTDEEQEVISKFLSALTE   142
                 T   GN  TDEEQ+ ++  +  L E
Sbjct   117  NDISETI--FGN-LTDEEQKQLANLMEKLVE   144
```

>**ref|NP_266864.1|** [G] transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=291

GENE ID: 1114333 rmaB | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 51.2 bits (121), Expect = 4e-08, Method: Compositional matrix adjust.
 Identities = 35/91 (38%), Positives = 50/91 (54%), Gaps = 3/91 (3%)

```
Query   52   TNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHH   111
             TNA+IAE L I P++VT  +K+L+E E++    +  ND+RV    LT+K    +   T H
Sbjct   57   TNAEIAELLDIKPSSVTAQVKQLEEAEMVIRKQDENDKRVSRIFLTDKGREAQETRDTMH   116

Query   112  EKTLSTYQELGNKFTDEEQEVISKFLSALTE   142
                 T   GN  TDEEQE ++  +  L E
Sbjct   117  NDISETI--FGN-LTDEEQEQLAFLMEKLVE   144
```

>**ref|YP_808147.1|** [G] transcriptional regulator [Lactococcus lactis subsp. cremoris
SK11]
Length=169

GENE ID: 4432499 LACR_0099 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 50.4 bits (119), Expect = 7e-08, Method: Compositional matrix adjust.
 Identities = 27/98 (27%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query   41   HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA   100
             HIL  L ++  T  ++A KL ++    VT+A++ L + + + + +A ND++ + + +T K
Sbjct   53   HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG   112

Query   101  VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS   138
             + VA  H    H+       ++  +K+ + E+ +I  FLS
Sbjct   113  LKVASIHDKMHKIMDLKLGQIFDKYNENEKSIILNFLS   150
```

>**ref|YP_001031482.1|** [G] MarR family transcriptional regulator [Lactococcus lactis subsp.
cremoris MG1363]
Length=172

GENE ID: 4798609 rmaD | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 49.3 bits (116), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query   41   HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA   100
             HIL  L ++  T  ++A KL ++    VT+A++ L + + + + +A ND++ + + +T K
Sbjct   56   HILSALTKKDLTGIELATKLSVTRGGVTRAVQNLIKHQFLTTYQADNDKKKIYYHITTKG   115

Query   101  VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS   138
             + VA  H    H+       ++  +K+ + + ++ +I  FLS
Sbjct   116  LKVASIHDKMHKIMDLKLGQIFDKYNENDKSIILNFLS   153
```

\>ref|NP_266269.1| transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=163

 GENE ID: 1113719 rmaD | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 46.2 bits (108), Expect = 1e-06, Method: Compositional matrix adjust.
 Identities = 26/98 (26%), Positives = 55/98 (56%), Gaps = 0/98 (0%)

```
Query   41  HILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA   100
            HIL  L ++   T  ++A KL ++     VT+A++ L + + + + ++ +D++ + + LT K
Sbjct   53  HILSALTKEDLTGIELATKLSVTRGGVTRAVQNLIKYQFLTTYQSESDKKKIFYHLTVKG   112

Query   101 VPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLS   138
            VA  H    H+        ++ +K+ ++E+ +I  FLS
Sbjct   113 RKVATIHDKMHKIMDIRLGQIFDKYNEQEKSIILSFLS   150
```


\>ref|NP_267628.1| transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=356

 GENE ID: 1115129 rmaC | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 41.2 bits (95), Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 29/100 (29%), Positives = 52/100 (52%), Gaps = 1/100 (1%)

```
Query   25  LLGKCESDVKLTSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSS   83
            +  K E    + T+ ++M+L +   + +++ +LKI  AAVT+ LK L+E+ L+K
Sbjct   20  MTAKFEKSTGYSITRYQLMMILKCKGRCSQSQLQNELKIDSAAVTRHLKLLEEKNLVKRE   79

Query   84  RATNDERVVLWSLTEKAVPVAKEHATHHEKTLSTYQELGN   123
            R  + R V   +T+KA      A  H+ +L   Q++ N
Sbjct   80  RNKENNREVFVEITDKAKNDLALCAKKHDDSLDESQQILN   119
```


\>ref|YP_001032345.1| MarR family transcriptional regulator [Lactococcus lactis subsp.
cremoris MG1363]
Length=139

 GENE ID: 4798214 rmaC | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 38.9 bits (89), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 25/92 (27%), Positives = 49/92 (53%), Gaps = 1/92 (1%)

```
Query   25  LLGKCESDVKLTSTQEHILMLL-AEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSS   83
            +  K E    + T+ ++M+L +   +      +LKI  AAVT+ LK L+E+ L+K
Sbjct   20  MTAKFEKSTGFSITRYQLMMILKCKGRCSQTQLQNELKIDSAAVTRHLKLLEEKNLVKRQ   79

Query   84  RATNDERVVLWSLTEKAVPVAKEHATHHEKTL   115
            R  ++ R V   +T++A     +  A  H+ ++
Sbjct   80  RNKDNNREVFVEITDEAKADLERCAREHDNSV   111
```


\>ref|YP_808479.1| transcriptional regulator [Lactococcus lactis subsp. cremoris
SK11]
Length=166

 GENE ID: 4433047 LACR_0453 | transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 37.0 bits (84), Expect = 9e-04, Method: Compositional matrix adjust.
 Identities = 31/111 (27%), Positives = 54/111 (48%), Gaps = 13/111 (11%)

```
Query   39  QEHILMLLAEQISTNAKIAEK-----LKISPAAVTKALKKLQEQELIKSSRATNDERVVL   93
            Q  IL +L E    N+K+ +K      L + P + ++ +KKL++++ I    +  D+R  +
Sbjct   43  QGQILNILME----NSKMTQKNLVAQLDMRPQSASEMIKKLEKKQFISRQKDAQDKRGFI   98

Query   94  WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF   144
            SLTEK  V +E A   E         +   FT+EE+  ++ +  L  E
Sbjct   99  ISLTEKGKAVLEESAEQTELVPG----IMTSFTEEEKIEFARLIGKLQSEL   145
```


\>ref|NP_266463.1| MarR family transcriptional regulator [Lactococcus lactis subsp.
lactis Il1403]
Length=159

 GENE ID: 1113917 napB | MarR family transcriptional regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 36.2 bits (82), Expect = 0.001, Method: Compositional matrix adjust.
 Identities = 23/84 (27%), Positives = 46/84 (54%), Gaps = 0/84 (0%)

```
Query   55  KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKT   114
```

```
                  K+A  L ++  A +K  KKL ++ L++S +   +++ + + LT++    +   H + H+K
Sbjct   60        KLAHHLYMTRGAASKIAKKLLKKNLVESYQIPQNKKEIYFRLTKEGQEINDRHESLHQKF  119

Query  115        LSTYQELGNKFTDEEQEVISKFLS  138
                     Q + ++ TDE     I KFL+
Sbjct  120        SEKDQVIFDELTDESVSNILKFLN  143
```

>ref|NP_266747.1| 🅖 transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=143

GENE ID: 1114211 rmaJ | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 35.8 bits (81), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 23/65 (35%), Positives = 33/65 (50%), Gaps = 0/65 (0%)

```
Query   42        ILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAV  101
                  I ML  E   T  K+ E+L +     ++ LK+L+ + I   R+  DER V  LT+K
Sbjct   40        IAMLAIENKMTINKLGEELSLDSGTLSPLLKRLEAKGYIVRKRSDKDERSVELFLTDKGA  99

Query  102        PVAKE  106
                  V KE
Sbjct  100        QVKKE  104
```

>ref|YP_001031675.1| 🅖 MarR family transcriptional regulator [Lactococcus lactis subsp.
cremoris MG1363]
Length=157

GENE ID: 4798013 napB | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 35.4 bits (80), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 23/83 (27%), Positives = 45/83 (54%), Gaps = 0/83 (0%)

```
Query   55        KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKT  114
                  K+A  L ++  A +K  KKL ++ LI+S +   +++ + + LT++    + H + H+K
Sbjct   58        KLAHHLYMTRGAASKIAKKLLKKNLIESYQIPQNKKEIYFRLTKEGQQINDRHESLHQKF  117

Query  115        LSTYQELGNKFTDEEQEVISKFL  137
                     Q + ++ TDE     I +FL
Sbjct  118        SQNDQVIFDELTDEAVSNILEFL  140
```

>ref|NP_266898.1| 🅖 MarR family transcriptional regulator [Lactococcus lactis subsp.
lactis Il1403]
Length=158

GENE ID: 1114368 rmaA | MarR family transcriptional regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 35.4 bits (80), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 22/66 (33%), Positives = 36/66 (54%), Gaps = 3/66 (4%)

```
Query   41        HILMLLAEQISTNA---KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLT  97
                  +L L++  I N    +I + L I  ++V +A+K L E+E +   R   D+RV   SLT
Sbjct   42        QLLCLISLYIKDNQSQEQITDDLSIDKSSVHRAIKGLIEKEYVSRVRDEKDKRVYRVSLT  101

Query   98        EKAVPV  103
                  +KA +
Sbjct  102        QKARDI  107
```

>ref|YP_808372.1| 🅖 MarR family transcriptional regulator [Lactococcus lactis subsp.
cremoris SK11]
Length=157

GENE ID: 4434175 LACR_0343 | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 35.4 bits (80), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 23/83 (27%), Positives = 45/83 (54%), Gaps = 0/83 (0%)

```
Query   55        KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEKT  114
                  K+A  L ++  A +K  KKL ++ LI+S +   +++ + + LT++    + H + H+K
Sbjct   58        KLAHHLYMTRGAASKIAKKLLKKNLIESYQIPQNKKEIYFRLTKEGQQINDRHESLHQKF  117

Query  115        LSTYQELGNKFTDEEQEVISKFL  137
                     Q + ++ TDE     I +FL
Sbjct  118        SQNDQVIFDELTDEAVSNILEFL  140
```

>ref|YP_001031774.1| 🅖 transcriptional regulator [Lactococcus lactis subsp. cremoris
MG1363]
Length=166

GENE ID: 4798362 llmg_0424 | transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

```
 Score = 35.0 bits (79),  Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 29/111 (26%), Positives = 53/111 (47%), Gaps = 13/111 (11%)

Query  39   QEHILMLLAEQISTNAKIAEK-----LKISPAAVTKALKKLQEQELIKSSRATNDERVVL   93
            Q  IL +L E   N+K+ +K     L + P + ++ +KKL++++ I   +   D+R +
Sbjct  43   QGQILNILME----NSKMTQKNLVAQLDMRPQSASEMIKKLEKKQFISRQKDAQDKRGFI   98

Query  94   WSLTEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTEEF          144
            SLTEK  V +E     +     +     FT+EE+   ++ +  L  E
Sbjct  99   ISLTEKGKAVLEESTEQTGRVPG----IMTSFTEEEKIEFARLIGKLQSEL          145
```

>ref|YP_001031879.1| putative transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=156

GENE ID: 4796958 llmg_0529 | putative transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

```
 Score = 32.3 bits (72),  Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 18/62 (29%), Positives = 38/62 (61%), Gaps = 7/62 (11%)

Query  33   VKLTSTQE---HILMLLAE----QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRA   85
            +KL+S  E   ++L++LA      +  ++  +A +LK+SP+ + K +K L ++ L++S+
Sbjct  1    MKLSSGWEQSVYVLLILARLPENRTMSSIALANRLKVSPSYLKKIIKSLVDEGLLRSTTG   60

Query  86   TN   87
            N
Sbjct  61   KN   62
```

>ref|YP_808573.1| BadM/Rrf2 family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=156

GENE ID: 4433945 LACR_0579 | BadM/Rrf2 family transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

```
 Score = 32.3 bits (72),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 18/62 (29%), Positives = 38/62 (61%), Gaps = 7/62 (11%)

Query  33   VKLTSTQE---HILMLLAE----QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRA   85
            +KL+S  E   ++L++LA      +  ++  +A +LK+SP+ + K +K L ++ L++S+
Sbjct  1    MKLSSGWEQSVYVLLILARLPENRTMSSIALANRLKVSPSYLKKIIKSLVDEGLLRSTTG   60

Query  86   TN   87
            N
Sbjct  61   KN   62
```

>ref|NP_266714.1| hypothetical protein L153086 [Lactococcus lactis subsp. lactis Il1403]
Length=156

GENE ID: 1114177 yffB | hypothetical protein
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

```
 Score = 32.3 bits (72),  Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 18/62 (29%), Positives = 38/62 (61%), Gaps = 7/62 (11%)

Query  33   VKLTSTQE---HILMLLAE----QISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRA   85
            +KL+S  E   ++L++LA      +  ++  +A +LK+SP+ + K +K L ++ L++S+
Sbjct  1    MKLSSGWEQSVYVLLILARLPENRTMSSIALANRLKVSPSYLKKIIKSLVDEGLLRSTPG   60

Query  86   TN   87
            N
Sbjct  61   KN   62
```

>ref|YP_001033090.1| MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=160

GENE ID: 4798315 rmaA | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

```
 Score = 31.6 bits (70),  Expect = 0.031, Method: Compositional matrix adjust.
 Identities = 29/107 (27%), Positives = 52/107 (48%), Gaps = 10/107 (9%)

Query  41   HILMLLAEQISTNA---KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLT   97
            +L L++  I  N    +I + L I  ++V +A++ L E+E +    R  +D+R   SLT
Sbjct  42   QLLCLISLYIKDNQSQEQITDDLSIDKSSVHRAIRSLIEKEYVVRVRDEHDKRAYRVSLT  101

Query  98   EKAVPVAK--EHATHHEKTLSTYQELGNKFTDEEQEVISKFLSALTE          142
            +KA +    E  T  + L      L        +E+E+  K L+ +T+
```

Sbjct 102 KKARAIQSQIEEMTKERENL-----LSEGIDPKEKEIAFKVLNQMTQ 143

>ref|YP_808765.1| MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=155

 GENE ID: 4432345 LACR_0786 | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 31.6 bits (70), Expect = 0.034, Method: Compositional matrix adjust.
 Identities = 20/65 (30%), Positives = 36/65 (55%), Gaps = 3/65 (4%)

Query 42   ILMLLAEQISTNA---KIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTE 98
            +L L++   I N   +I + L I ++V +A++ L E+E +   R +D+R   SLT+
Sbjct 43   LLCLISLYIKDNQSQEQITDDLSIDKSSVHRAIRSLIEKEYVVRVRDEHDKRAYRVSLTK 102

Query 99   KAVPV 103
            KA +
Sbjct 103 KARAI 107

>ref|YP_808795.1| MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
 ref|YP_001033061.1| MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=146

 GENE ID: 4433123 LACR_0820 | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 31.2 bits (69), Expect = 0.044, Method: Compositional matrix adjust.
 Identities = 19/57 (33%), Positives = 31/57 (54%), Gaps = 3/57 (5%)

Query 56   IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHE 112
            IA+ K++ + +T L +L+++ I+ R+T D RV   LT K +   ATH E
Sbjct 57   IAKNQKLALSTITITLNRLEDKGYIERKRSTADRRVTHIILTSKGDELC---ATHRE 110

>ref|NP_266926.1| MarR family transcriptional regulator [Lactococcus lactis subsp. lactis Il1403]
Length=146

 GENE ID: 1114397 rmaG | MarR family transcriptional regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 31.2 bits (69), Expect = 0.045, Method: Compositional matrix adjust.
 Identities = 19/57 (33%), Positives = 31/57 (54%), Gaps = 3/57 (5%)

Query 56   IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHE 112
            IA+ K++ + +T L +L+++ I+ R+T D RV   LT K +   ATH E
Sbjct 57   IAKNQKLALSTITITLNRLEDKGYIERKRSTADRRVTHIILTSKGDELC---ATHRE 110

>ref|YP_001032909.1| MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=154

 GENE ID: 4797429 rmaH | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 28.9 bits (63), Expect = 0.18, Method: Compositional matrix adjust.
 Identities = 24/85 (28%), Positives = 41/85 (48%), Gaps = 1/85 (1%)

Query 54   AKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEK 113
            +KIA+   S A +   L L+ + LI   + D R+L ++T+K VA+E
Sbjct 51   SKIAKFTHTSTARIATILNNLESKNLITREISRTDRRKILVAITDKGRRVAEEIRVEACS 110

Query 114 TLS-TYQELGNKFTDEEQEVISKFL 137
            L+ ++E+G + T+   E   FL
Sbjct 111 NLARVFKEMGEERTESFIENFKMFL 135

>ref|YP_001032520.1| MarR family transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=127

 GENE ID: 4797914 rmaX | MarR family transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 28.1 bits (61), Expect = 0.31, Method: Compositional matrix adjust.
 Identities = 24/86 (27%), Positives = 36/86 (41%), Gaps = 6/86 (6%)

Query 54   AKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEK 113
            + IA +   S A V   L L+E++I   + D R+L LT+K   KE T
Sbjct 29   SDIARYIGASTARVANILNNLEEKGMISREISREDRRKILVFLTDKGRKETKERRTR--- 85

```
Query  114  TLSTYQELGNKFTDEEQEVISKFLSA  139
                T  + N F   +E   +F+ A
Sbjct   86  ---TITRISNVFEAMGEERTQQFIEA  108
```

>ref|**NP_267064.1**| 🅖 transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=154

GENE ID: 1114538 rmaH | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.35, Method: Compositional matrix adjust.
Identities = 23/85 (27%), Positives = 41/85 (48%), Gaps = 1/85 (1%)

```
Query  54  AKIAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHATHHEK  113
           +KIA+    S A +   L  L+ + L+    + D R +L ++T+K   VA+E
Sbjct  51  SKIAKFTHTSTARIATILNNLESKNLVTREISRTDRRKILVAITDKGRHVAEEIRVEACS  110

Query  114  TLS-TYQELGNKFTDEEQEVISKFL  137
            L+  ++E+G + T+   E    FL
Sbjct  111  NLARVFEEMGEERTESFIENFKLFL  135
```

>ref|**YP_001032533.1**| 🅖 transcriptional regulator [Lactococcus lactis subsp. cremoris MG1363]
Length=217

GENE ID: 4798916 llmg_1224 | transcriptional regulator
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.38, Method: Compositional matrix adjust.
Identities = 14/33 (42%), Positives = 24/33 (72%), Gaps = 1/33 (3%)

```
Query  48  EQISTNAKIAEKLKISPAAVTKALKKLQEQELI  80
           E +S NA IA+KL +S + T+ +K+L ++EL+
Sbjct  23  ESVSINA-IAQKLSVSSPSATEMIKRLAKKELV  54
```

>ref|**YP_809312.1**| 🅖 Mn-dependent transcriptional regulator [Lactococcus lactis subsp. cremoris SK11]
Length=217

GENE ID: 4432558 LACR_1369 | Mn-dependent transcriptional regulator
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 28.1 bits (61), Expect = 0.38, Method: Compositional matrix adjust.
Identities = 14/33 (42%), Positives = 24/33 (72%), Gaps = 1/33 (3%)

```
Query  48  EQISTNAKIAEKLKISPAAVTKALKKLQEQELI  80
           E +S NA IA+KL +S + T+ +K+L ++EL+
Sbjct  23  ESVSINA-IAQKLSVSSPSATEMIKRLAKKELV  54
```

>ref|**NP_267461.1**| 🅖 transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=156

GENE ID: 1114954 rmaF | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 27.7 bits (60), Expect = 0.42, Method: Compositional matrix adjust.
Identities = 15/45 (33%), Positives = 24/45 (53%), Gaps = 0/45 (0%)

```
Query  56  IAEKLKISPAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKA  100
           + E L IS A+  + L+E+EL+     ND+R+    LTE+
Sbjct  63  LLEVLDISKQALNGPMNDLKEKELVHFKPNENDKRIKQLYLTEQG  107
```

>ref|**NP_267696.1**| 🅖 transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=148

GENE ID: 1115197 rmaI | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 27.3 bits (59), Expect = 0.61, Method: Compositional matrix adjust.
Identities = 32/142 (22%), Positives = 60/142 (42%), Gaps = 18/142 (12%)

```
Query  11   LGTIMQFAENKHEILLGKCESDVKLTSTQEHILMLLAEQISTNAK-------IAEKLKIS  63
            +G +++ A N+        + + LT  Q  IL  L  Q   ++       I + I
Sbjct  8    IGRLLKVASNQMSREFDNFAAQLDLTGQQMSILDFLGNQSEEDSGKEISQTMIELEFNIR  67

Query  64   PAAVTKALKKLQEQELIKSSRATNDERVVLWSLTEKAVPVAKEHAT----HHEKTLSTYQ  119
            +  T+ L++++++LIK  + D R    LTE+     E  T     H++K L+
Sbjct  68   RSTTTEILQRMEKRQLIKRKASPTDARQKSVELTEEGKQYLPEIRTYIQGHNQKALAG--  125

Query  120  ELGNKFTDEEQEVISKFLSALT  141
            + EE  + KFL+  +
Sbjct  126  -----LSAEEIAAVEKFLNNFS  142
```

>**ref|NP_266753.1|** G NADPH-flavin oxidoreductase [Lactococcus lactis subsp. lactis Il1403]
Length=216

 GENE ID: 1114217 yfiJ | NADPH-flavin oxidoreductase
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 27.3 bits (59), Expect = 0.67, Method: Compositional matrix adjust.
 Identities = 11/29 (37%), Positives = 18/29 (62%), Gaps = 0/29 (0%)

Query 109 THHEKTLSTYQELGNKFTDEEQEVISKFL 137
            +HH+K+   QE+ N T   +E ++KFL
Sbjct 180 SHHQKSTDWTQEMSNFLTKPRREDVAKFL 208

>**ref|NP_267412.1|** G metalloregulator [Lactococcus lactis subsp. lactis Il1403]
Length=217

 GENE ID: 1114905 ymiA | metalloregulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 26.6 bits (57), Expect = 1.1, Method: Compositional matrix adjust.
 Identities = 13/31 (41%), Positives = 23/31 (74%), Gaps = 1/31 (3%)

Query 50   ISTNAKIAEKLKISPAAVTKALKKLQEQELI 80
            +S NA IA+KL +S + T+ +K+L ++EL+
Sbjct 25   VSINA-IAQKLSVSSPSATEMIKRLAKKELV 54

>**ref|YP_001031697.1|** G putative cobalt ABC transporter ATP-binding protein [Lactococcus lactis subsp. cremoris MG1363]
Length=565

 GENE ID: 4798558 cbiO | putative cobalt ABC transporter ATP-binding protein
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 26.2 bits (56), Expect = 1.2, Method: Compositional matrix adjust.
 Identities = 12/27 (44%), Positives = 17/27 (62%), Gaps = 0/27 (0%)

Query 55   KIAEKLKISPAAVTKALKKLQEQELIK 81
            ++A K ISP ++TKA   Q QE +K
Sbjct 537 QLARKADISPISLTKAFINFQNQERLK 563

>**ref|NP_266873.1|** G quinone oxidoreductase [Lactococcus lactis subsp. lactis Il1403]
Length=328

 GENE ID: 1114342 qor | quinone oxidoreductase
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 25.4 bits (54), Expect = 2.4, Method: Compositional matrix adjust.
 Identities = 10/19 (52%), Positives = 11/19 (57%), Gaps = 0/19 (0%)

Query 109 THHEKTLSTYQELGNKFTD 127
            HHEK +   ELG KF D
Sbjct 193 NHHEKLVPQVHELGFKFVD 211

>**ref|NP_268402.1|** G alkylphosphonate uptake protein [Lactococcus lactis subsp. lactis Il1403]
Length=114

 GENE ID: 1115923 phnA | alkylphosphonate uptake protein
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 25.4 bits (54), Expect = 2.4, Method: Compositional matrix adjust.
 Identities = 14/41 (34%), Positives = 19/41 (46%), Gaps = 0/41 (0%)

Query 97   TEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFL 137
            T K + + E+   T   E GN+FT EE E   KF+
Sbjct 3   TPKCIHCSSEYTYELSDTSFGCSECGNEFTLEEIEAAGKFI 43

>**ref|YP_808209.1|** G transcriptional repressor CodY [Lactococcus lactis subsp. cremoris SK11]
Length=262

 GENE ID: 4434653 LACR_0168 | transcriptional repressor CodY
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 24.6 bits (52), Expect = 3.4, Method: Compositional matrix adjust.
 Identities = 10/27 (37%), Positives = 19/27 (70%), Gaps = 0/27 (0%)

Query 56   IAEKLKISPAAVTKALKKLQEQELIKS 82
            IA+K+ I+ + + AL+KL+ +I+S

Sbjct 210 IADKIGITRSVIVNALRKLESAGVIES 236

>ref|YP_001031533.1| G transcriptional repressor CodY [Lactococcus lactis subsp. cremori
MG1363]
Length=262

 GENE ID: 4797198 codY | transcriptional repressor CodY
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 24.6 bits (52), Expect = 3.4, Method: Compositional matrix adjust.
 Identities = 10/27 (37%), Positives = 19/27 (70%), Gaps = 0/27 (0%)

Query 56   IAEKLKISPAAVTKALKKLQEQELIKS 82
            IA+K+ I+ + + AL+KL+ +I+S
Sbjct 210 IADKIGITRSVIVNALRKLESAGVIES 236

>ref|NP_266317.1| G transcriptional repressor CodY [Lactococcus lactis subsp. lactis
Il1403]
Length=262

 GENE ID: 1113769 codY | transcriptional repressor CodY
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 24.6 bits (52), Expect = 3.5, Method: Compositional matrix adjust.
 Identities = 10/27 (37%), Positives = 19/27 (70%), Gaps = 0/27 (0%)

Query 56   IAEKLKISPAAVTKALKKLQEQELIKS 82
            IA+K+ I+ + + AL+KL+ +I+S
Sbjct 210 IADKIGITRSVIVNALRKLESAGVIES 236

>ref|NP_266838.1| G intercellular adhesion protein [Lactococcus lactis subsp. lactis
Il1403]
Length=276

 GENE ID: 1114306 icaB | intercellular adhesion protein
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 24.6 bits (52), Expect = 3.6, Method: Compositional matrix adjust.
 Identities = 14/46 (30%), Positives = 21/46 (45%), Gaps = 0/46 (0%)

Query 43   LMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQELIKSSRATND 88
            L L Q   K+ + + S +   K +KK+ E L+ S   TND
Sbjct 126 LDLPFTQFIITGKVGQTIDGSQMSTWKEIKKMNENPLVTSGLHTND 171

>ref|NP_266710.1| G transcription regulator [Lactococcus lactis subsp. lactis Il1403]
Length=247

 GENE ID: 1114173 yfeA | transcription regulator
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 24.6 bits (52), Expect = 3.6, Method: Compositional matrix adjust.
 Identities = 16/44 (36%), Positives = 25/44 (56%), Gaps = 5/44 (11%)

Query 35   LTSTQEHILMLLAEQIS-----TNAKIAEKLKISPAAVTKALKK 73
            LTS + +I   L E +   T A+IAE +SP+++ + LKK
Sbjct 4   LTSVEIYIWNYLEENKAKIIQMTVAQIAESAHVSPSSIIRTLKK 47

>ref|NP_266438.1| G amino acid amidohydrolase [Lactococcus lactis subsp. lactis Il1403]
Length=384

 GENE ID: 1113892 yciA | amino acid amidohydrolase
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 24.6 bits (52), Expect = 4.1, Method: Compositional matrix adjust.
 Identities = 11/41 (26%), Positives = 17/41 (41%), Gaps = 7/41 (17%)

Query 8   DQFLGT-------IMQFAENKHEILLGKCESDVKLTSTQEH 41
            D+F G   + A N+H + G CE ++   T H
Sbjct 147 DEFYGLHVRPDLKVGDIATNQHTLFAGTCEVELSFIGTGGH 187

>ref|YP_808446.1| G lysyl-tRNA synthetase [Lactococcus lactis subsp. cremoris SK11]
Length=494

 GENE ID: 4433352 lysS | lysyl-tRNA synthetase
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 24.6 bits (52), Expect = 4.3, Method: Composition-based stats.
 Identities = 12/34 (35%), Positives = 20/34 (58%), Gaps = 0/34 (0%)

Query 98   EKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE 131
            E+A +AKEH H EK ++   + N+F ++ E

Sbjct 340   EEATALAKEHDIHVEKHFTSVGHIINEFFEKYVE 373

>**ref|YP_001031741.1|** 🅖 lysyl-tRNA synthetase [Lactococcus lactis subsp. cremoris MG1363]
Length=494

GENE ID: 4799123 lysS | lysyl-tRNA synthetase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 24.3 bits (51), Expect = 4.7, Method: Composition-based stats.
 Identities = 12/34 (35%), Positives = 20/34 (58%), Gaps = 0/34 (0%)

Query 98   EKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE 131
             E+A +AKEH H EK ++   + N+F ++ E
Sbjct 340   EEATALAKEHDIHVEKHFTSVGHIINEFFEKYVE 373

>**ref|NP_266529.1|** 🅖 lysyl-tRNA synthetase [Lactococcus lactis subsp. lactis Il1403]
Length=494

GENE ID: 1113984 lysS | lysyl-tRNA synthetase
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 24.3 bits (51), Expect = 4.7, Method: Composition-based stats.
 Identities = 12/34 (35%), Positives = 20/34 (58%), Gaps = 0/34 (0%)

Query 98   EKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQE 131
             E+A +AKEH H EK ++   + N+F ++ E
Sbjct 340   EEATALAKEHDIHVEKHFTSVGHIINEFFEKYVE 373

>**ref|YP_001031907.1|** 🅖 NADPH-flavin oxidoreductase [Lactococcus lactis subsp. cremoris MG1363]
Length=251

GENE ID: 4798593 llmg_0559 | NADPH-flavin oxidoreductase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 24.3 bits (51), Expect = 5.2, Method: Compositional matrix adjust.
 Identities = 9/29 (31%), Positives = 19/29 (65%), Gaps = 0/29 (0%)

Query 109   THHEKTLSTYQELGNKFTDEEQEVISKFL 137
             +HH+K+ + QE+ + T+ +E ++ FL
Sbjct 215   SHHQKSTNWSQEMSDFLTNPRREDLTDFL 243

>**ref|YP_808603.1|** 🅖 NADPH-flavin oxidoreductase [Lactococcus lactis subsp. cremoris SK11]
Length=251

GENE ID: 4433732 LACR_0613 | NADPH-flavin oxidoreductase
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

 Score = 24.3 bits (51), Expect = 5.5, Method: Compositional matrix adjust.
 Identities = 9/29 (31%), Positives = 19/29 (65%), Gaps = 0/29 (0%)

Query 109   THHEKTLSTYQELGNKFTDEEQEVISKFL 137
             +HH+K+ + QE+ + T+ +E ++ FL
Sbjct 215   SHHQKSTNWSQEMSDFLTNPRREDLADFL 243

>**ref|NP_268293.1|** 🅖 exported serine protease [Lactococcus lactis subsp. lactis Il1403]
Length=408

GENE ID: 1115813 htrA | exported serine protease
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

 Score = 23.9 bits (50), Expect = 6.1, Method: Compositional matrix adjust.
 Identities = 17/59 (28%), Positives = 34/59 (57%), Gaps = 5/59 (8%)

Query 15   MQFAENKHEI--LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKAL 71
             + FA   +++ ++ K E+D K++   I M+   Q+STN   + +LK+ P++VT +
Sbjct 271   LGFAIPSNDVVNIINKLEADGKISRPALGIRMVDLSQLSTND--SSQLKL-PSSVTGGV 326

>**ref|YP_001033660.1|** 🅖 housekeeping protease [Lactococcus lactis subsp. cremoris MG1363]
Length=407

GENE ID: 4797497 htrA | housekeeping protease
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

 Score = 23.9 bits (50), Expect = 6.5, Method: Compositional matrix adjust.
 Identities = 17/59 (28%), Positives = 34/59 (57%), Gaps = 5/59 (8%)

Query 15   MQFAENKHEI--LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKAL 71
             + FA   +++ ++ K E+D K++   I M+   Q+STN   + +LK+ P++VT +
Sbjct 270   LGFAIPSNDVVNIINKLETDGKISRPALGIRMVDLSQLSTND--SSQLKL-PSSVTGGV 325

>ref|YP_811995.1| **G** trypsin-like serine protease [Lactococcus lactis subsp. cremoris SK11]
Length=407

GENE ID: 4432303 LACR_2439 | trypsin-like serine protease
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

Score = 23.9 bits (50), Expect = 6.6, Method: Compositional matrix adjust.
Identities = 17/59 (28%), Positives = 34/59 (57%), Gaps = 5/59 (8%)

```
Query  15   MQFAENKHEI--LLGKCESDVKLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKAL   71
            + FA     +++   ++ K E+D K++     I M+   Q+STN   + +LK+ P++VT  +
Sbjct  270  LGFAIPSNDVVNIINKLETDGKISRPALGIRMVDLSQLSTND--SSQLKL-PSSVTGGV   325
```

>ref|NP_268332.1| **G** hypothetical protein L35545 [Lactococcus lactis subsp. lactis Il1403]

ref|YP_812032.1| **G** hypothetical protein LACR_2483 [Lactococcus lactis subsp. cremoris SK11]

ref|YP_001033699.1| **G** hypothetical protein llmg_2459 [Lactococcus lactis subsp. cremori MG1363]
Length=82

GENE ID: 1115852 ywfB | hypothetical protein
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 7.5, Method: Compositional matrix adjust.
Identities = 13/29 (44%), Positives = 14/29 (48%), Gaps = 0/29 (0%)

```
Query  97   TEKAVPVAKEHATHHEKTLSTYQELGNKF   125
            TE    AKE A  +E  L  YQ L  KF
Sbjct  34   TEDGKKEAKEAAIRYESRLDAYQFLQGKF   62
```

>ref|NP_268337.1| **G** hypothetical protein L39650 [Lactococcus lactis subsp. lactis Il1403]
Length=926

GENE ID: 1115857 ywfG | hypothetical protein
[Lactococcus lactis subsp. lactis Il1403] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 7.7, Method: Composition-based stats.
Identities = 11/25 (44%), Positives = 13/25 (52%), Gaps = 0/25 (0%)

```
Query  118  YQELGNKFTDEEQEVISKFLSALTE   142
            Y E G KF D+ Q  I +    LTE
Sbjct  557  YPEDGTKFADDPQHYIVRLKHGLTE   581
```

>ref|YP_001032772.1| **G** superfamily II DNA/RNA helicase [Lactococcus lactis subsp. cremoi MG1363]
Length=430

GENE ID: 4797767 comFA | superfamily II DNA/RNA helicase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 7.8, Method: Compositional matrix adjust.
Identities = 17/46 (36%), Positives = 26/46 (56%), Gaps = 1/46 (2%)

```
Query  34   KLTSTQEHILMLLAEQISTNAKIAEKLKISPAAVTKALKKLQEQEL   79
            KLT  QE I   L +QI+ N K+  +  ++ A  T+ +  +L EQ L
Sbjct  105  KLTENQEKISNALCQQITNNQKLLVQ-AVTGAGKTEMIYQLIEQIL   149
```

>ref|YP_001033122.1| **G** quinone oxidoreductase [Lactococcus lactis subsp. cremoris MG136:
Length=328

GENE ID: 4798878 qor | quinone oxidoreductase
[Lactococcus lactis subsp. cremoris MG1363] (10 or fewer PubMed links)

Score = 23.5 bits (49), Expect = 9.3, Method: Compositional matrix adjust.
Identities = 9/18 (50%), Positives = 10/18 (55%), Gaps = 0/18 (0%)

```
Query  110  HHEKTLSTYQELGNKFTD   127
            HHE  +    ELG KF D
Sbjct  194  HHENLVPQVHELGFKFVD   211
```

>ref|YP_808733.1| **G** quinone oxidoreductase [Lactococcus lactis subsp. cremoris SK11]
Length=328

GENE ID: 4432226 LACR_0751 | quinone oxidoreductase
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

```
Score = 23.5 bits (49),  Expect = 9.3, Method: Compositional matrix adjust.
Identities = 9/18 (50%), Positives = 10/18 (55%), Gaps = 0/18 (0%)

Query  110  HHEKTLSTYQELGNKFTD  127
            HHE  +     ELG KF D
Sbjct  194  HHENLVPQVHELGFKFVD  211
```

>**ref|YP_796521.1|** hypothetical protein LACR_C57 [Lactococcus lactis subsp. cremoris SK11]
Length=330

  GENE ID: 4405852 LACR_C57 | hypothetical protein
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

```
 Score = 23.5 bits (49),  Expect = 9.5, Method: Compositional matrix adjust.
 Identities = 11/33 (33%), Positives = 22/33 (66%), Gaps = 0/33 (0%)

Query  53   NAKIAEKLKISPAAVTKALKKLQEQELIKSSRA  85
            N K  ++L  S +  ++A  K+Q Q+L+K+S++
Sbjct  189  NIKDTQELDFSSSNFSEAQLKVQNQDLVKNSKS  221
```

>**ref|YP_812095.1|** hypothetical protein LACR_2554 [Lactococcus lactis subsp. cremoris SK11]
Length=114

  GENE ID: 4432134 LACR_2554 | hypothetical protein
[Lactococcus lactis subsp. cremoris SK11] (10 or fewer PubMed links)

```
 Score = 23.1 bits (48),  Expect = 10.0, Method: Compositional matrix adjust.
 Identities = 13/41 (31%), Positives = 18/41 (43%), Gaps = 0/41 (0%)

Query  97   TEKAVPVAKEHATHHEKTLSTYQELGNKFTDEEQEVISKFL  137
            T K +  + E+          E GN+FT EE E   KF+
Sbjct  3    TPKCIHCSSEYTYELSDMSFGCSECGNEFTLEEIEAAGKFI  43
```

Select All Get selected sequences Distance tree of results